

Sequence Listing R10901 Corrected.txt
SEQUENCE LISTING

<110> O'Donnell, Michael E.
Yurieva, Olga

<120> ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
USE THEREOF

<130> 22221/1030

<140> 09/716,964

<141> 2000-11-21

<150> 09/642,218

<151> 2000-08-18

<150> 09/057,416

<151> 1998-04-08

<150> 60/143,202

<151> 1997-04-08

<160> 212

<170> Patent in Ver. 2.1

<210> 1

<211> 2007

<212> DNA

<213> Thermus thermophilus

<400> 1

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actagacctg tgagcccgct ctaccgcgcg ttccgcccc tcacctcca ggaggtgggtg 180
gggcaggagc acgtgaagga gccctctctc aaggccatcc gggaggggag gctctccag 240
gctacctctc tctccggggt caggggcggt ggcaagacca ccacggcgag gctctctgc 300
atggcggtgg ggtgccagg ggaaagcccc ccttgccggg tctgccccca ctgcaggcg 360
gtgcagaggg gcgccccacc ggacgtgggt gacattgacg ccgcacgcaa caactccgtg 420
gaggacgtgc gggagctgag ggaagggatc cacctcgccc cctctctgc ccccaggaa 480
gtcttctatc tggacgaggc ccacatgctc tccaaaagcg ccttcaacgc cctctcaag 540
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atgcccccca ccatctcttc ccgcacccag cacttcggtc tccgcgcct caccggagg 660
gagatcgctt ttaagctccg gcgcacctctg gaggccgtgg ggccggaggc ggaggaggag 720
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gagcgtcttc tctctggga agcccccctc acccggaagg aggtggagcg cgccctaggc 840
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gaggccctgg gctctgcgcg gcgcctctac ggggaagggt acgcccgcag gagcctggtc 960
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gagcgcctgg ccgcgcgcgc cgacgcctta agcctggagg tggcctctct ggaggcgga 1140
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cccaagccgg aaagcccccc gaccccggaa ccccaaggc ccgaggaggc gcccgacctg 1260
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cccgcccgcc cccacatccc tgaagcgccc gaacccccg gccctccga ggaggaggta 1560

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gaggcgaggg aagcgggcga ggaggcccg gaggaggcct tgaggcggtt ggtccgcctc 1620
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cccttgagcc aagacgagat agggggtact ggtatataat gggggcatga cgcgaccac 1740
cgacctcgga caagagacgg tggacaacat cctcaagcgc ctccgcgcga ttgaggggca 1800
ggtgcggggg ctccagaaga tggtgccga gggccgcccc tgcgacgagg tctcaccaca 1860
gatgaccgcc accaagaagg ccatggaggg ggcggccacc ctgatcctcc acgagttctc 1920
gaacgtctgc gcgcggagg tctcggagg caaggtgaac cccaagaagc ccgaggagat 1980
cgccaccatg ctgaagaact tcatcta 2007

```

<210> 2
 <211> 529
 <212> PRT
 <213> Thermus thermophilus

<400> 2
 Met Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1 5 10 15
 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
 20 25 30
 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35 40 45
 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60
 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80
 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
 85 90 95
 Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
 100 105 110
 Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
 115 120 125
 Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
 130 135 140
 His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
 145 150 155 160
 Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
 165 170 175
 Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
 180 185 190
 Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
 195 200 205
 Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
 210 215 220
 Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro

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225 230 235 240
 Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
 245 250 255
 Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
 260 265 270
 Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
 275 280 285
 Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
 290 295 300
 Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
 305 310 315 320
 Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
 325 330 335
 Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
 340 345 350
 Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
 355 360 365
 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
 370 375 380
 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 385 390 395 400
 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 405 410 415
 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
 420 425 430
 Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
 435 440 445
 Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro
 450 455 460
 Glu Ala Pro Ala Pro Pro Gly Pro Pro Glu Glu Glu Val Glu Ala Glu
 465 470 475 480
 Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg
 485 490 495
 Leu Leu Gly Gly Arg Val Leu Trp Val Arg Arg Pro Arg Thr Arg Glu
 500 505 510
 Ala Pro Glu Glu Glu Pro Leu Ser Gln Asp Glu Ile Gly Gly Thr Gly
 515 520 525
 Ile

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<210> 3
 <211> 1590
 <212> DNA
 <213> *Thermus thermophilus*

<400> 3
 gtgagcgccc tctaccgcgg ctcccgcccc ctccacctcc aggagggtgt ggggcaggag 60
 cactgtgaagg agccccctct caaggccatc cgggagggga ggctcgccca ggctacctc 120
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 ggggtgccagg gggaagaccc ccttgcggg gtctgcctcc actgccagcc ggtgcagagg 240
 ggcccccacc cggacgttgt ggaattgac gccgccagca acaactccgt ggaggacgtg 300
 cgggagctga gggaaaggat ccacctcgcc cccctctctg cccccaggaa ggtcttcac 360
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 tttaaagctc ggccatctct ggaggccgtg gggcgggagg cggaggagga ggcctctctc 600
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 ggggacgggg tggccgagat cgccgcctcc ctgcgagagg ggaaaacggc ggaggccctg 780
 ggctctcgcc ggccctctta cggggaaggg tacgccccga ggagccttgt ctccggcctt 840
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 gccccgcccc aggcctctat cgccgccatg accgcccgtg acgaggccat gaagcgccctc 960
 gccccgcgct ccgacgcctt aagcctggag gtggccctcc tggaggcgcc ggagggcctc 1020
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 gaaagccccc cgacccccga acccccaagg cccgaggagg cggccgacct cggggagcgg 1140
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 ccggagggtc gggaaggcca gctctgcctc gctttccccc aggacaagge cttccactac 1260
 cgcaaggctc cggaaacagaa ggtgaggtc cctccccctg cccaggccca ttccggggtg 1320
 gaggagggtg tctctgctct ggaggagaaa aaaaaaagcc tgagcccaag gcccccggcg 1380
 gccccacttc ctgaagcgcc cgcacccccg ggccctcccg aggaggaggt agaggcgag 1440
 gaagcgcgcg aggaggcccc ggaggaggcc ttgaggcggg ttgtccgcct cctggggggg 1500
 cgggtgctct ggtgcggcg gcccaaggac cgggaggcgc cggaggagga acccctgagc 1560
 caagacgaga tagggggatc tggatatata 1590

<210> 4
 <211> 464
 <212> PRT
 <213> *Thermus thermophilus*

<400> 4
 Met Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1 5 10 15
 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
 20 25 30
 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35 40 45
 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Gln Gln
 50 55 60
 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80
 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
 85 90 95

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Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
100                               105                               110

Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
115                               120                               125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
130                               135                               140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
145                               150                               155                               160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
165                               170                               175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
180                               185                               190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
195                               200                               205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
210                               215                               220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
225                               230                               235                               240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
245                               250                               255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
260                               265                               270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
275                               280                               285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
290                               295                               300

Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
305                               310                               315                               320

Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
325                               330                               335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
340                               345                               350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
355                               360                               365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
370                               375                               380

Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
385                               390                               395                               400

Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys

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405

410

415

Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
 420 425 430
 Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
 435 440 445
 Gly Glu Lys Lys Lys Pro Glu Pro Lys Ala Pro Pro Gly Pro Thr Ser
 450 455 460

<210> 5

<211> 454

<212> PRT

<213> Thermus thermophilus

<400> 5

Met Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1 5 10 15
 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
 20 25 30
 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35 40 45
 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60
 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80
 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
 85 90 95
 Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
 100 105 110
 Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
 115 120 125
 Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
 130 135 140
 His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
 145 150 155 160
 Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
 165 170 175
 Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
 180 185 190
 Glu Ala Glu Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly
 195 200 205

Sequence_Listing_R10901_Corrected.txt

```

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
210                215                220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
225                230                235                240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
                245                250                255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
                260                265                270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
275                280                285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
290                295                300

Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
305                310                315                320

Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
                325                330                335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
340                345                350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
355                360                365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
370                375                380

Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
385                390                395                400

Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
405                410                415

Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
420                425                430

Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
435                440                445

Gly Glu Lys Lys Lys Ala
450

```

<210> 6

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6

Sequence_Listing_R10901_Corrected.txt 32
cgcaagcttc acgcstacct sttctccggs ac

<210> 7
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 7
His Ala Tyr Leu Phe Ser Gly Thr
1 5

<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 8
cgcggaattcg tgctcsggsg gctcctcsag sgtc 34

<210> 9
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 9
Lys Thr Leu Glu Glu Pro Pro Glu His
1 5

<210> 10
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
gcgcggatcc ggagggagaa aaaaaaagcc tcagccca 38

<210> 11
<211> 38
<212> DNA
<213> Artificial Sequence

<220>


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<223> Description of Artificial Sequence: primer

<400> 11
gcgcggaatcc ggaggagag aagaaaagcc tcagccca 38

<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 12
gaattaaatt cgcgcttcgg gaggtggg 28

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13
gcgcgaaattc gcgcttcggg aggtggg 27

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
gcgcgaattc ggcgccttca ggaggtggg 29

<210> 15
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
gtggtgcata tggtagcgc cctctaccgc c 31

<210> 16
<211> 31
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: primer

<400> 16
gtgggtggtcg acccaggagg gccacctcca g                               31

<210> 17
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (2)
<223> X is any aa at position 2

<220>
<221> PEPTIDE
<222> (3)
<223> X is any aa at position 3

<220>
<221> PEPTIDE
<222> (5)
<223> X is any aa at position 5

<400> 17
Gly Xaa Xaa Gly Xaa Gly Lys Thr
 1                               5

<210> 18
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 18
Lys Pro Asp Pro Lys Ala Pro Pro Gly Pro Thr Ser
 1                               5                               10

<210> 19
<211> 180
<212> PRT
<213> Escherichia coli

<400> 19
Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
 1                               5                               10                               15

Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu
 20                               25                               30

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Sequence_Listing_R10901_Corrected.txt

```

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
   35                               40                               45
Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
   50                               55                               60
Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
   65                               70                               75                               80
Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
   85                               90                               95
Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
  100                               105                               110
Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
  115                               120                               125
His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
  130                               135                               140
Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
  145                               150                               155                               160
Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
  165                               170                               175
Ala Leu Asp Val
  180

```

<210> 20

<211> 180

<212> PRT

<213> Bacillus subtilis

<400> 20

```

Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
   1                               5                               10                               15
Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
   20                               25                               30
Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
   35                               40                               45
Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
   50                               55                               60
Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys
   65                               70                               75                               80
Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala
   85                               90                               95
Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
  100                               105                               110

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Sequence_Listing_R10901_Corrected.txt

Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val
115 120 125

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His
145 150 155 160

Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys
165 170 175

Arg Ile Thr Ser
180

<210> 21

<211> 294

<212> PRT

<213> Escherichia coli

<400> 21

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu
20 25 30

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Val Glu Gln Ile Arg His Gln Leu Glu His Ile Leu Asn
180 185 190

Glu Glu His Ile Ala His Glu Pro Arg Ala Leu Gln Leu Leu Ala Arg

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200 205

195

Ala Ala Glu Gly Ser Leu Arg Asp Ala Leu Ser Leu Thr Asp Gln Ala
210 215 220
Ile Ala Ser Gly Asp Gly Gln Val Ser Thr Gln Ala Val Ser Ala Met
225 230 235 240
Leu Gly Thr Leu Asp Asp Asp Gln Ala Leu Ser Leu Val Glu Ala Met
245 250 255
Val Glu Ala Asn Gly Glu Arg Val Met Ala Leu Ile Asn Glu Ala Ala
260 265 270
Ala Arg Gly Ile Glu Trp Glu Ala Leu Leu Val Glu Met Leu Gly Leu
275 280 285
Leu His Arg Ile Ala Met
290

<210> 22

<211> 294

<212> PRT

<213> Haemophilus influenzae

<400> 22

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Lys Thr Phe Ala
1 5 10 15
Asp Val Val Gly Gln Glu His Ile Ile Thr Ala Leu Ala Asn Gly Leu
20 25 30
Lys Asp Asn Arg Leu His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45
Val Gly Lys Thr Ser Ile Ala Arg Leu Phe Ala Lys Gly Leu Asn Cys
50 55 60
Val His Gly Val Thr Ala Thr Pro Cys Gly Glu Cys Glu Asn Cys Lys
65 70 75 80
Ala Ile Glu Gln Gly Asn Phe Ile Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95
Ser Arg Thr Lys Val Glu Asp Thr Arg Glu Leu Leu Asp Asn Val Gln
100 105 110
Tyr Lys Pro Val Val Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125
His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140
Glu Pro Pro Glu Tyr Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160
Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Sequence_Listing_R10901_Corrected.txt

Ala Leu Asp Glu Thr Gln Ile Ser Gln His Leu Ala His Ile Leu Thr
180 185 190

Gln Glu Asn Ile Pro Phe Glu Asp Pro Ala Leu Val Lys Leu Ala Lys
195 200 205

Ala Ala Gln Gly Ser Ile Arg Asp Ser Leu Ser Leu Thr Asp Gln Ala
210 215 220

Ile Ala Met Gly Asp Arg Gln Val Thr Asn Asn Val Val Ser Asn Met
225 230 235 240

Leu Gly Leu Leu Asp Asp Asn Tyr Ser Val Asp Ile Leu Tyr Ala Leu
245 250 255

His Gln Gly Asn Gly Glu Leu Leu Met Arg Thr Leu Gln Arg Val Ala
260 265 270

Asp Ala Ala Gly Asp Trp Asp Lys Leu Leu Gly Glu Cys Ala Glu Lys
275 280 285

Leu His Gln Ile Ala Leu
290

<210> 23
<211> 294
<212> PRT
<213> Bacillus subtilis

<400> 23
Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
20 25 30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
50 55 60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys
65 70 75 80

Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala
85 90 95

Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
100 105 110

Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val
115 120 125

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Sequence_Listing_R10901_Corrected.txt

Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His
 145 150 155 160
 Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys
 165 170 175
 Arg Ile Thr Ser Gln Ala Ile Val Gly Arg Met Asn Lys Ile Val Asp
 180 185 190
 Ala Glu Gln Leu Gln Val Glu Glu Gly Ser Leu Glu Ile Ile Ala Ser
 195 200 205
 Ala Ala His Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala
 210 215 220
 Ile Ser Phe Ser Gly Asp Ile Leu Lys Val Glu Asp Ala Leu Leu Ile
 225 230 235 240
 Thr Gly Ala Val Ser Gln Leu Tyr Ile Gly Lys Leu Ala Lys Ser Leu
 245 250 255
 His Asp Lys Asn Val Ser Asp Ala Leu Glu Thr Leu Asn Glu Leu Leu
 260 265 270
 Gln Gln Gly Lys Asp Pro Ala Lys Leu Ile Glu Asp Met Ile Phe Tyr
 275 280 285
 Phe Arg Asp Met Leu Leu
 290

<210> 24

<211> 300

<212> PRT

<213> *Caulobacter crescentus*

<400> 24

Asp Ala Tyr Thr Val Leu Ala Arg Lys Tyr Arg Pro Arg Thr Phe Glu
 1 5 10 15
 Asp Leu Ile Gly Gln Glu Ala Met Val Arg Thr Leu Ala Asn Ala Phe
 20 25 30
 Ser Thr Gly Arg Ile Ala His Ala Phe Met Leu Thr Gly Val Arg Gly
 35 40 45
 Val Gly Lys Thr Thr Thr Ala Arg Leu Leu Ala Arg Ala Leu Asn Tyr
 50 55 60
 Glu Thr Asp Thr Val Lys Gly Pro Ser Val Asp Leu Thr Thr Glu Gly
 65 70 75 80
 Tyr His Cys Arg Ser Ile Ile Glu Gly Arg His Met Asp Val Leu Glu
 85 90 95
 Leu Asp Ala Ala Ser Arg Thr Lys Val Asp Glu Met Arg Glu Leu Leu
 100 105 110
 Asp Gly Val Arg Tyr Ala Pro Val Glu Ala Arg Tyr Lys Val Tyr Ile

Sequence_Listing_R10901_Corrected.txt

115

120

125

Ile Asp Glu Val His Met Leu Ser Thr Ala Ala Phe Asn Ala Leu Leu
130 135 140

Lys Thr Leu Glu Glu Pro Pro His Ala Lys Phe Ile Phe Ala Thr
145 150 155 160

Thr Glu Ile Arg Lys Val Pro Val Thr Ile Leu Ser Arg Cys Gln Arg
165 170 175

Phe Asp Leu Arg Arg Val Glu Pro Asp Val Leu Val Lys His Phe Asp
180 185 190

Arg Ile Ser Ala Lys Glu Gly Ala Arg Ile Glu Met Asp Ala Leu Ala
195 200 205

Leu Ile Ala Arg Ala Ala Glu Gly Ser Val Arg Asp Gly Leu Ser Leu
210 215 220

Leu Asp Gln Ala Ile Val Gln Thr Glu Arg Gly Gln Thr Val Thr Ser
225 230 235 240

Thr Val Val Arg Asp Met Leu Gly Leu Ala Asp Arg Ser Gln Thr Ile
245 250 255

Ala Leu Tyr Glu His Val Met Ala Gly Lys Thr Lys Asp Ala Leu Glu
260 265 270

Gly Phe Arg Ala Leu Trp Gly Phe Gly Ala Asp Pro Ala Val Val Met
275 280 285

Leu Asp Val Leu Asp His Cys His Ala Ser Ala Val
290 295 300

<210> 25

<211> 260

<212> PRT

<213> Mycoplasma genitalium

<400> 25

Met His Gln Val Phe Tyr Gln Lys Tyr Arg Pro Ile Asn Phe Lys Gln
1 5 10 15

Thr Leu Gly Gln Glu Ser Ile Arg Lys Ile Leu Val Asn Ala Ile Asn
20 25 30

Arg Asp Lys Leu Pro Asn Gly Tyr Ile Phe Ser Gly Glu Arg Gly Thr
35 40 45

Gly Lys Thr Thr Phe Ala Lys Ile Ile Ala Lys Ala Ile Asn Cys Leu
50 55 60

Asn Trp Asp Gln Ile Asp Val Cys Asn Ser Cys Asp Val Cys Lys Ser
65 70 75 80

Ile Asn Thr Asn Ser Ala Ile Asp Ile Val Glu Ile Asp Ala Ala Ser
85 90 95

Sequence_Listing_R10901_Corrected.txt

```

Lys Asn Gly Ile Asn Asp Ile Arg Glu Leu Val Glu Asn Val Phe Asn
100                               105                               110

His Pro Phe Thr Phe Lys Lys Lys Val Tyr Ile Leu Asp Glu Ala His
115                               120                               125

Met Leu Thr Thr Gln Ser Trp Gly Gly Leu Leu Lys Thr Leu Glu Glu
130                               135                               140

Ser Pro Pro Tyr Val Leu Phe Ile Phe Thr Thr Thr Glu Phe Asn Lys
145                               150                               155                               160

Ile Pro Leu Thr Ile Leu Ser Arg Cys Gln Ser Phe Phe Phe Lys Lys
165                               170                               175

Ile Thr Ser Asp Leu Ile Leu Glu Arg Leu Asn Asp Ile Ala Lys Lys
180                               185                               190

Glu Lys Ile Lys Ile Glu Lys Asp Ala Leu Ile Lys Ile Ala Asp Leu
195                               200                               205

Ser Gln Gly Ser Leu Arg Asp Gly Leu Ser Leu Leu Asp Gln Leu Ala
210                               215                               220

Ile Ser Leu Ile Val Lys Lys Leu Val Leu Leu Met Leu Lys Lys His
225                               230                               235                               240

Leu Ile Ser Leu Ile Glu Met Gln Asn Leu Leu Leu Leu Lys Gln Phe
245                               250                               255

Tyr Gln Glu Ile
260

<210> 26
<211> 289
<212> PRT
<213> Thermus thermophilus

<400> 26
Val Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
1                               5                               10                               15

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
20                               25                               30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
35                               40                               45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
50                               55                               60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
65                               70                               75                               80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
85                               90                               95

```

Sequence_Listing_R10901_Corrected.txt

```

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
    100                      105                      110
Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
    115                      120                      125
Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
    130                      135                      140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
    145                      150                      155                      160
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
    165                      170                      175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
    180                      185                      190
Glu Ala Glu Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly
    195                      200                      205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
    210                      215                      220
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
    225                      230                      235                      240
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
    245                      250                      255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
    260                      265                      270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
    275                      280                      285

```

Tyr

```

<210> 27
<211> 101
<212> RNA
<213> Thermus thermophilus

```

```

<400> 27
guccugagg gagaaaaaaa aagccugagc ccaaggcccc gcccgcccc accuccugaa 60
gcccgcgcac ccccgggccc ucccgaggag gagguagagg c 101

```

```

<210> 28
<211> 11
<212> PRT
<213> Thermus thermophilus

```

```

<400> 28
Val Leu Glu Gly Glu Lys Lys Ser Leu Ser Pro
    1                      5                      10

```

Sequence_Listing_R10901_Corrected.txt

<210> 29
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <221> unsure
 <222> {6}
 <223> N at position 6 is either G or C

<220>
 <221> unsure
 <222> {12}
 <223> N at position 12 is either G or C

<220>
 <221> unsure
 <222> {21}
 <223> N at position 21 is either G or C

<400> 29
 cagcgtacc tnttctcgg nac 23

<210> 30
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <221> unsure
 <222> {7}
 <223> N at position 7 is either G or C

<220>
 <221> unsure
 <222> {10}
 <223> N at position 10 is either G or C

<220>
 <221> unsure
 <222> {19}
 <223> N at position 19 is either G or C

<220>
 <221> unsure
 <222> {22}
 <223> N at position 22 is either G or C

<400> 30
 gtgctcnggn ggctctctnt cngtc 25

Sequence_Listing_R10901_Corrected.txt

```

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
gtgggatccg tggttctgga tctcgatgaa gaa          33

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
gtgggatcca cggstctstcs gagcagaag          29

<210> 33
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 33
gcgggatcct caacgaggac ctctccatct tcaa          34

<210> 34
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 34
gcgggatcct tctcgctcsag sgtsagsgcg tcgta          35

<210> 35
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 35
gggaaggacc agcggtact cccctgctc ctagggtgtg          39

```

Sequence_Listing_R10901_Corrected.txt

```

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 36
gtgtggatcc ttattcttsc ccatsgc                27

<210> 37
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 37
caccgattcc agtgggtgcot aggtgtg                27

<210> 38
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 38
caacacctgg tgtccagga gcctgtgctt                30

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 39
ccagaatcgt ctgctggtcg tag                    23

<210> 40
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 40

```

agcaccctgg aggagcttc

19

<210> 41
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
catgtcgtac tgggtgtac

19

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> {7}
<223> N at position 7 is A, C, G, or T

<220>
<221> unsure
<222> {8}
<223> N at position 8 is A, C, G, or T

<220>
<221> unsure
<222> {13}
<223> N at position 13 is A, C, G, or T

<220>
<221> unsure
<222> {14}
<223> N at position 14 is A, C, G, or T

<400> 42
gtggtstnsg acnnsagagac sacsggg

27

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> {8}
<223> N at position 8 is A, C, G, or T

Sequence_Listing_R10901_Corrected.txt

```

<220>
<221> unsure
<222> {9}
<223> N at position 9 is A, C, G, or T

<220>
<221> unsure
<222> {17}
<223> N at position 17 is A, C, G, or T

<220>
<221> unsure
<222> {18}
<223> N at position 18 is A, C, G, or T

<400> 43
gaasccsnng tcgaasnng cgttgtg 27

<210> 44
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
cggggatcca cctcaatcac ctctgtg 27

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 45
cggggatccg ccaccttgcg gctccgggtg 30

<210> 46
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 46
gcgctctaga cgagttccca aagcgtgcgg t 31

<210> 47
<211> 25
<212> DNA

```

```

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 47
cgcgtctaga tcacctgtat ccaga                25

<210> 48
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 48
ggggcgcata tgggtggtgt cctggacctg gag        33

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 49
cgcgtctaga tcacctgtat ccaga                25

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 50
gtscstgtsa agacscactt                      20

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 51
sagsagsgcg ttgaasgtgt g                    21

<210> 52
<211> 22

```


Sequence_listing_R10901_Corrected.txt

```

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  primer

<400> 52
ctcgttggtg aaagtttcg tg                22

<210> 53
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  primer

<400> 53
cgtccagttc atcgccggaa agga            24

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  primer

<400> 54
tctggcaaca cgttctggag cacatcc        27

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  primer

<400> 55
tgctggcggtt catcttcagg atg           23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  primer

<400> 56
catctgaag atgaacgcca gca             23

<210> 57

```

Sequence_Listing_R10901_Corrected.txt

```

<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 57
aggttatcca caggggtcat gtgca                25

<210> 58
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
gtgtgtcata tgaacataac gggtcccaa            29

<210> 59
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 59
gcgcgaattc tccttgtgg aaggttag              29

<210> 60
<211> 13
<212> PRT
<213> Thermus thermophilus

<400> 60
Arg Val Glu Leu Asp Tyr Asp Ala Leu Thr Leu Asp Asp
 1             5             10

<210> 61
<211> 14
<212> PRT
<213> Thermus thermophilus

<400> 61
Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys
 1             5             10

<210> 62
<211> 8
<212> PRT
<213> Thermus thermophilus

```

Sequence_Listing_R10901_Corrected.txt

<400> 62

Phe Phe Ile Glu Ile Gln Asn His
1 5

<210> 63

<211> 8

<212> PRT

<213> Thermus thermophilus

<400> 63

Tyr Asp Ala Leu Thr Leu Asp Asp
1 5

<210> 64

<211> 6

<212> PRT

<213> Thermus thermophilus

<400> 64

Ala Met Gly Lys Lys Lys
1 5

<210> 65

<211> 9

<212> PRT

<213> Thermus thermophilus

<400> 65

Phe Asn Lys Ser His Ser Ala Ala Tyr
1 5

<210> 66

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<220>

<221> PEPTIDE

<222> (3)

<223> Xaa at position 3 is undefined

<220>

<221> PEPTIDE

<222> (5)

<223> Xaa at position 5 is undefined

<400> 66

Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

Sequence_Listing_R10901_Corrected.txt

<210> 67
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<220>
 <221> PEPTIDE
 <222> (4)
 <223> Xaa at position 4 is undefined

<220>
 <221> PEPTIDE
 <222> (7)
 <223> Xaa at position 7 is undefined

<400> 67
 His Asn Ala Xaa Phe Asp Xaa Gly Phe
 1 5

<210> 68
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<220>
 <221> PEPTIDE
 <222> (3)
 <223> Xaa at position 3 is undefined

<220>
 <221> PEPTIDE
 <222> (5)
 <223> Xaa at position 5 is undefined

<400> 68
 Val Val Xaa Asp Xaa Glu Thr Thr Gly
 1 5

<210> 69
 <211> 7
 <212> PRT
 <213> Thermus thermophilus

<400> 69
 Val Leu Val Lys Thr His Leu
 1 5

<210> 70
 <211> 6
 <212> PRT

Sequence_Listing_R10901_Corrected.txt

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 70

His Arg Ala Leu Tyr Asp
1 5

<210> 71

<211> 7

<212> PRT

<213> Thermus thermophilus

<400> 71

His Thr Phe Asn Ala Leu Leu
1 5

<210> 72

<211> 34

<212> PRT

<213> Escherichia coli

<400> 72

Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg Gly Leu Pro
20 25 30

Val Val

<210> 73

<211> 34

<212> PRT

<213> Vibrio cholerae

<400> 73

Asp His Phe Tyr Leu Glu Leu Ile Arg Thr Gly Arg Ala Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Phe Ala Leu Asp Val Ala Glu Gln Tyr Asp Leu Pro
20 25 30

Val Val

<210> 74

<211> 34

<212> PRT

<213> Haemophilus influenzae

<400> 74

Asp His Phe Tyr Leu Ala Leu Ser Arg Thr Gly Arg Pro Asn Glu Glu

Sequence_Listing_R10901_Corrected.txt

1 5 10 15
Arg Tyr Ile Gln Ala Ala Leu Lys Leu Ala Glu Arg Cys Asp Leu Pro
 20 25 30

Leu Val

<210> 75

<211> 34

<212> PRT

<213> Rickettsia prowazekii

<400> 75

Asp Arg Phe Tyr Phe Glu Ile Met Arg His Asp Leu Pro Glu Glu Gln
1 5 10 15

Phe Ile Glu Asn Ser Tyr Ile Gln Ile Ala Ser Glu Leu Ser Ile Pro
 20 25 30

Ile Val

<210> 76

<211> 34

<212> PRT

<213> Helicobacter pylori

<400> 76

Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp Gln Arg
1 5 10 15

Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly Leu Lys
 20 25 30

Ile Ile

<210> 77

<211> 34

<212> PRT

<213> Synechocystis sp.

<400> 77

Asp Asp Tyr Tyr Leu Glu Ile Gln Asp His Gly Ser Val Glu Asp Arg
1 5 10 15

Leu Val Asn Ile Asn Leu Val Lys Ile Ala Gln Glu Leu Asp Ile Lys
 20 25 30

Ile Val

<210> 78

<211> 34

Sequence_Listing_R10901_Corrected.txt

<212> PRT

<213> *Mycobacterium tuberculosis*

<400> 78

Asp Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Thr Ile Glu Arg
1 5 10 15

Arg Val Arg Asp Gly Leu Leu Glu Ile Gly Arg Ala Leu Asn Ile Pro
20 25 30

Pro Leu

<210> 79

<211> 46

<212> PRT

<213> *Escherichia coli*

<400> 79

Asn Lys Arg Arg Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 80

<211> 46

<212> PRT

<213> *Vibrio cholerae*

<400> 80

Asn Pro Arg Leu Lys Lys Ala Gly Lys Pro Pro Val Arg Ile Glu Ala
1 5 10 15

Ile Pro Leu Asp Asp Ala Arg Ser Phe Arg Asn Leu Gln Asp Ala Lys
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu
35 40 45

<210> 81

<211> 46

<212> PRT

<213> *Haemophilus influenzae*

<400> 81

Asn Val Arg Met Val Arg Glu Gly Lys Pro Arg Val Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Pro Glu Ser Phe Glu Leu Leu Lys Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp

35

40

45

<210> 82

<211> 46

<212> PRT

<213> *Rickettsia prowazekii*

<400> 82

Cys	Lys	Lys	Leu	Lys	Glu	Gln	Gly	Ile	Lys	Ile	Asp	Phe	Asp	Asp
1				5				10					15	

Met	Thr	Phe	Asp	Asp	Lys	Lys	Thr	Tyr	Gln	Met	Leu	Cys	Lys	Gly	Lys
			20					25					30		

Gly	Val	Gly	Val	Phe	Gln	Phe	Glu	Ser	Ile	Gly	Met	Lys	Asp
		35					40					45	

<210> 83

<211> 45

<212> PRT

<213> *Helicobacter pylori*

<400> 83

Leu	Lys	Ile	Ile	Lys	Thr	Gln	His	Lys	Ile	Ser	Val	Asp	Phe	Leu	Ser
1				5					10					15	

Leu	Asp	Met	Asp	Asp	Pro	Lys	Val	Tyr	Lys	Thr	Ile	Gln	Ser	Gly	Asp
			20					25					30		

Thr	Val	Gly	Ile	Phe	Gln	Ile	Glu	Ser	Gly	Met	Phe	Gln
		35					40					45

<210> 84

<211> 46

<212> PRT

<213> *Synechocystis* sp.

<400> 84

Gln	Glu	Arg	Lys	Ala	Leu	Gln	Ile	Arg	Ala	Arg	Thr	Gly	Ser	Lys	Lys
1				5					10					15	

Leu	Pro	Asp	Asp	Val	Lys	Lys	Thr	His	Lys	Leu	Leu	Glu	Ala	Gly	Asp
			20				25						30		

Leu	Glu	Gly	Ile	Phe	Gln	Leu	Glu	Ser	Gln	Gly	Met	Lys	Gln
		35					40					45	

<210> 85

<211> 46

<212> PRT

<213> *Mycobacterium tuberculosis*

<400> 85

Ile	Asp	Asn	Val	Arg	Ala	Asn	Arg	Gly	Ile	Asp	Leu	Asp	Leu	Glu	Ser
1				5					10					15	

Sequence_Listing_R10901_Corrected.txt

Val Pro Leu Asp Asp Lys Ala Thr Tyr Glu Leu Leu Gly Arg Gly Asp
20 25 30

Thr Leu Gly Val Phe Gln Leu Asp Gly Gly Pro Met Arg Asp
35 40 45

<210> 86

<211> 3729

<212> DNA

<213> Thermus thermophilus

<400> 86

```

atggggcggg agctcgcgtt cgcccaacct caccagcaca cccagttctc cctcctggag 60
ggggcggcga agctttccga cctcctcaag tgggtcaagg agaagacccc cgaggacccc 120
gccttggcca gtaccagacca cggcaacctc ttcggggcgg tggagtctta caaagaagggc 180
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gcgcgcgccc acgaggtcct cctcgccatc cagtccaaga gcaccttggc cgaccccggg 720
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cggggggaga ccaagggggt ctccagctg gagtccgggg gatatccgcg cactctccgc 2040
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cccatggagc acatccccac ctacatccgc gcccaacgag gctcgagacc cctcgagacc 2160
agcagatttc cccacgcgca gaagtaccta aagccatcc ttgacgagac ctacggcatc 2220
cccgctacac agggagcagt catcgagatc gctcggggc tggcggggta ctccttgggc 2280
gaggcgaccc tctcgtcgcg gtccatgggg aagaagaagg ttgaggagat gaagtccacc 2340
cgggagcgct tcgtccaggg ggcacaaggaa agggcgctgc ccgaggagga ggcaccaaccg 2400
ctctttgca cgtctggagg cttcgccaac tacggcttca acaaatccca cctcgccgcc 2460
tacagactcc tctcctacca gaccgcttac gtgaagggccc actaccccgt ggagttcatg 2520
gccgcctccc tctcgttgga ggcggcacag tgcccgagta catccgcgac 2580
gcccgggcca tgggcataga ggtccttccc ccggacgtca accgctccgg gtttgaactc 2640
ctggtccagg gccggcgat ccttttcggc ctctcccggg tgaagaacct gggcgaggcg 2700

```

Sequence Listing R10901 Corrected.txt

```

ggggcggagg ccattctccg ggagcgggag cggggcggcc cctaccggag cctcggcgac 2760
ttctccaagc ggctggacga gaaggtgctc aacaagcgga cctcggagtc cctcatcaag 2820
ggggcggccc tggacggcgtt cggggaaagg ggcggcgtcc tgcctcctct ggaaggcgctc 2880
ctcaagtggg cggccgagaa cggggagaag gcccgctcgg gcatgatggg cctcttcagc 2940
gaagtggagg agccgccttt ggcgagggcc gcccccctgg acgagatcac ccggctccgc 3000
tacgagaagg aggcgccttt gatctacgtc tccggccacc ccatcttggc gtaccctggg 3060
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agcggcggga tgatggcccg ctctgtctct tccgaagaga cggggcgctc tgaggcgggtg 3240
gcatctggcc gggcctacga ccaggtctcc ccgaggtcca aggaggacac ccccgctgctc 3300
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cccttttgg

```

<210> 87

<211> 1245

<212> PRT

<213> Thermus thermophilus

<400> 87

Met Gly Arg Glu Leu Arg Phe Ala His Leu His Gln His Thr Gln Phe
1 5 10 15

Ser Leu Leu Asp Gly Ala Pro Lys Leu Ser Asp Leu Leu Lys Trp Val
20 25 30

Glu Glu Thr Thr Pro Glu Asp Pro Ala Leu Ala Met Thr Asp His Gly
35 40 45

Asn Leu Phe Gly Ala Val Glu Phe Tyr Lys Lys Ala Thr Glu Met Gly
50 55 60

Ile Lys Pro Ile Leu Gly Tyr Glu Ala Tyr Val Ala Ala Glu Ser Arg
65 70 75 80

Phe Asp Arg Lys Arg Gly Lys Gly Leu Asp Gly Gly Tyr Phe His Leu
85 90 95

Thr Leu Leu Ala Lys Asp Phe Thr Gly Tyr Gln Asn Leu Val Arg Leu
100 105 110

Ala Ser Arg Ala Tyr Leu Glu Gly Phe Tyr Glu Lys Pro Arg Ile Asp
115 120 125

Arg Glu Ile Leu Arg Glu His Ala Glu Gly Leu Ile Ala Leu Ser Gly
130 135 140

Cys Leu Gly Ala Glu Ile Pro Gln Phe Ile Leu Gln Asp Arg Leu Asp
145 150 155 160

Leu Ala Glu Ala Arg Leu Asn Glu Tyr Leu Ser Ile Phe Lys Asp Arg
165 170 175

Sequence Listing_R10901_Corrected.txt

Phe Phe Ile Glu Ile Gln Asn His Gly Leu Pro Glu Gln Lys Lys Val
180 185 190

Asn Glu Val Leu Lys Glu Phe Ala Arg Lys Tyr Gly Leu Gly Met Val
195 200 205

Ala Thr Asn Asp Gly His Tyr Val Arg Lys Glu Asp Ala Arg Ala His
210 215 220

Glu Val Leu Leu Ala Ile Gln Ser Lys Ser Thr Leu Asp Asp Pro Gly
225 230 235 240

Ala Leu Ala Leu Pro Cys Glu Glu Phe Tyr Val Lys Thr Pro Glu Glu
245 250 255

Met Arg Ala Met Phe Pro Glu Glu Glu Val Gly Gly Arg Ser Pro Leu
260 265 270

Thr Thr Pro Trp Arg Ser Pro His Val Gln Arg Gly Ala Ala Ile Gly
275 280 285

Thr Arg Trp Ser Thr Arg Ile Pro Arg Phe Pro Leu Pro Glu Gly Arg
290 295 300

Thr Glu Ala Gln Tyr Leu Met Glu Leu Thr Phe Lys Gly Leu Leu Arg
305 310 315 320

Arg Tyr Pro Asp Arg Ile Thr Glu Gly Phe Tyr Arg Glu Val Phe Arg
325 330 335

Leu Ser Gly Lys Leu Pro Pro His Gly Asp Gly Glu Ala Leu Ala Glu
340 345 350

Ala Leu Ala Gln Val Glu Arg Glu Ala Trp Glu Arg Leu Met Lys Ser
355 360 365

Leu Pro Pro Leu Ala Gly Val Lys Glu Trp Thr Ala Glu Ala Ile Phe
370 375 380

His Arg Ala Leu Tyr Glu Leu Ser Ala Ile Glu Arg Met Gly Phe Pro
385 390 395 400

Gly Leu Leu Pro His Arg Pro Gly Leu His Gln Leu Gly Pro Glu Lys
405 410 415

Gly Val Ser Val Gly Pro Gly Arg Gly Gly Ala Ala Gly Ser Leu Val
420 425 430

Ala Tyr Ala Val Gly Ile Thr Asn Ile Asp Pro Leu Arg Phe Gly Leu
435 440 445

Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp Ile
450 455 460

Asp Thr Asp Phe Ser Asp Arg Glu Arg Asp Arg Val Ile Gln Tyr Val
465 470 475 480

Arg Glu Arg Tyr Gly Glu Asp Lys Val Ala Gln Ile Gly Thr Leu Gly
485 490 495

Sequence_Listing_R10901_Corrected.txt

```

Ser Leu Ala Ser Lys Ala Ala Leu Lys Glu Val Ala Arg Val Tyr Gly
500 505 510

Ile Pro Arg Lys Lys Ala Glu Glu Leu Ala Lys Leu Ile Pro Val Gln
515 520 525

Phe Gly Lys Pro Lys Pro Leu Gln Glu Ala Ile Gln Val Val Pro Glu
530 535 540

Leu Arg Ala Glu Met Glu Lys Asp Pro Lys Val Arg Glu Val Leu Glu
545 550 555 560

Val Ala Met Arg Leu Glu Gly Leu Asn Arg His Ala Ser Val His Ala
565 570 575

Gly Arg Gly Gly Val Phe Ser Glu Pro Leu Thr Asp Leu Val Pro Leu
580 585 590

Cys Ala Thr Arg Lys Gly Gly Pro Tyr Thr Gln Tyr Asp Met Gly Ala
595 600 605

Val Glu Ala Leu Gly Leu Leu Lys Met Asp Phe Leu Gly Leu Arg Thr
610 615 620

Leu Thr Phe Leu Asp Glu Val Lys Arg Ile Val Lys Ala Ser Gln Gly
625 630 635 640

Val Glu Leu Asp Tyr Asp Ala Leu Pro Leu Asp Asp Pro Lys Thr Phe
645 650 655

Ala Leu Leu Ser Arg Gly Glu Thr Lys Gly Val Phe Gln Leu Glu Ser
660 665 670

Gly Gly Met Thr Ala Thr Leu Arg Gly Leu Lys Pro Arg Arg Phe Glu
675 680 685

Asp Leu Ile Ala Ile Leu Ser Leu Tyr Arg Pro Gly Pro Met Glu His
690 695 700

Ile Pro Thr Tyr Ile Arg Arg His His Gly Leu Glu Pro Val Ser Tyr
705 710 715 720

Ser Glu Phe Pro His Ala Glu Lys Tyr Leu Lys Pro Ile Leu Asp Glu
725 730 735

Thr Tyr Gly Ile Pro Val Tyr Gln Glu Gln Ile Met Gln Ile Ala Ser
740 745 750

Ala Val Ala Gly Tyr Ser Leu Gly Glu Ala Asp Leu Leu Arg Arg Ser
755 760 765

Met Gly Lys Lys Lys Val Glu Glu Met Lys Ser His Arg Glu Arg Phe
770 775 780

Val Gln Gly Ala Lys Glu Arg Gly Val Pro Glu Glu Glu Ala Asn Arg
785 790 795 800

Leu Phe Asp Met Leu Glu Ala Phe Ala Asn Tyr Gly Phe Asn Lys Ser

```

Sequence_Listing_R10901_Corrected.txt

```

805                               810                               815
His Ala Ala Ala Tyr Ser Leu Leu Ser Tyr Gln Thr Ala Tyr Val Lys
820                               825                               830
Ala His Tyr Pro Val Glu Phe Met Ala Ala Leu Leu Ser Val Glu Arg
835                               840                               845
His Asp Ser Asp Lys Val Ala Glu Tyr Ile Arg Asp Ala Arg Ala Met
850                               855                               860
Gly Ile Glu Val Leu Pro Pro Asp Val Asn Arg Ser Gly Phe Asp Phe
865                               870                               875                               880
Leu Val Gln Gly Arg Gln Ile Leu Phe Gly Leu Ser Ala Val Lys Asn
885                               890                               895
Val Gly Glu Ala Ala Ala Glu Ala Ile Leu Arg Glu Arg Glu Arg Gly
900                               905                               910
Gly Pro Tyr Arg Ser Leu Gly Asp Phe Leu Lys Arg Leu Asp Glu Lys
915                               920                               925
Val Leu Asn Lys Arg Thr Leu Glu Ser Leu Ile Lys Ala Gly Ala Leu
930                               935                               940
Asp Gly Phe Gly Glu Arg Ala Arg Leu Leu Ala Ser Leu Glu Gly Leu
945                               950                               955                               960
Leu Lys Trp Ala Ala Glu Asn Arg Glu Lys Ala Arg Ser Gly Met Met
965                               970                               975
Gly Leu Phe Ser Glu Val Glu Glu Pro Pro Leu Ala Glu Ala Ala Pro
980                               985                               990
Leu Asp Glu Ile Thr Arg Leu Arg Tyr Glu Lys Glu Ala Leu Gly Ile
995                               1000                               1005
Tyr Val Ser Gly His Pro Ile Leu Arg Tyr Pro Gly Leu Arg Glu Thr
1010                               1015                               1020
Ala Thr Cys Thr Leu Glu Glu Leu Pro His Leu Ala Arg Asp Leu Pro
1025                               1030                               1035                               1040
Pro Arg Ser Arg Val Leu Leu Ala Gly Met Val Glu Glu Val Val Arg
1045                               1050                               1055
Lys Pro Thr Lys Ser Gly Gly Met Met Ala Arg Phe Val Leu Ser Asp
1060                               1065                               1070
Glu Thr Gly Ala Leu Glu Ala Val Ala Phe Gly Arg Ala Tyr Asp Gln
1075                               1080                               1085
Val Ser Pro Arg Leu Lys Glu Asp Thr Pro Val Leu Val Leu Ala Glu
1090                               1095                               1100
Val Glu Arg Glu Glu Gly Gly Val Arg Val Leu Ala Gln Ala Val Trp
1105                               1110                               1115                               1120

```

Sequence_Listing_R10901_Corrected.txt

Thr Tyr Gln Glu Leu Glu Gln Val Pro Arg Ala Leu Glu Val Glu Val
 1125 1130 1135

Glu Ala Ser Leu Pro Asp Asp Arg Gly Val Ala His Leu Lys Ser Leu
 1140 1145 1150

Leu Asp Glu His Ala Gly Thr Leu Pro Leu Tyr Val Arg Val Gln Gly
 1155 1160 1165

Ala Phe Gly Glu Ala Leu Leu Ala Leu Arg Glu Val Arg Val Gly Glu
 1170 1175 1180

Glu Ala Leu Gly Ala Leu Glu Ala Ala Gly Phe Pro Ala Tyr Leu Leu
 1185 1190 1195 1200

Pro Asn Arg Glu Val Ser Pro Arg Leu Thr Gly Ser Gly Gly Pro Arg
 1205 1210 1215

Gly Arg Ala Leu Ser Thr Gly Leu Ala Leu Lys Thr Tyr Pro Ile Ala
 1220 1225 1230

Leu Pro Gly Gly Asn Glu Ala Leu Ala Arg Pro Leu Leu
 1235 1240 1245

<210> 88

<211> 198

<212> PRT

<213> Thermus thermophilus

<400> 88

Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu Glu
 1 5 10 15

Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu Gly
 20 25 30

Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly Leu
 35 40 45

Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg Arg
 50 55 60

Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala Arg
 65 70 75 80

Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala Pro
 85 90 95

Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp Ala
 100 105 110

Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg Pro
 115 120 125

Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp Ser
 130 135 140

Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly Leu

Sequence_Listing_R10901_Corrected.txt

145 150 155 160
 Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His Arg
 165 170 175
 Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val Tyr
 180 185 190
 Tyr Met Leu Thr Ser Gly
 195

<210> 89
 <211> 182
 <212> PRT
 <213> Deinococcus radiodurans

<220>
 <221> PEPTIDE
 <222> (79)
 <223> X at position 79 is undefined

<400> 89
 Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe
 1 5 10 15
 Ser Pro Ala Ser Ala Ala Ile Val Glu Ile Gly Ala Val Arg Ile Val
 20 25 30
 Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro
 35 40 45
 Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg
 50 55 60
 Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala Xaa Lys
 65 70 75 80
 Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val
 85 90 95
 Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu
 100 105 110
 Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln
 115 120 125
 Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val
 130 135 140
 Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg
 145 150 155 160
 Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu
 165 170 175
 Glu Leu Leu Gly Glu Arg
 180

Sequence_Listing_R10901_Corrected.txt

```

<210> 90
<211> 201
<212> PRT
<213> Bacillus subtilis

<400> 90
His Gly Ile Lys Met Ile Tyr Gly Met Glu Ala Asn Leu Val Asp Asp
 1           5           10           15

Gly Val Pro Ile Ala Tyr Asn Ala Ala His Arg Leu Leu Glu Glu Glu
          20           25           30

Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val Tyr
          35           40           45

Asp Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Gly Gly Glu Ile
          50           55           60

Ile Asp Lys Phe Glu Ala Phe Ala Asn Pro His Arg Pro Leu Ser Ala
          65           70           75           80

Thr Ile Ile Glu Leu Thr Gly Ile Thr Asp Asp Met Leu Gln Asp Ala
          85           90           95

Pro Asp Val Val Asp Val Ile Arg Asp Phe Arg Glu Trp Ile Gly Asp
          100          105          110

Asp Ile Leu Val Ala His Asn Ala Ser Phe Asp Met Gly Phe Leu Asn
          115          120          125

Val Ala Tyr Lys Lys Leu Leu Glu Val Glu Lys Ala Lys Asn Pro Val
          130          135          140

Ile Asp Thr Leu Glu Leu Gly Arg Phe Leu Tyr Pro Glu Phe Lys Asn
          145          150          155          160

His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
          165          170          175

His His Arg Ala Ile Tyr Asp Thr Glu Ala Thr Ala Tyr Leu Leu Leu
          180          185          190

Lys Met Leu Lys Asp Ala Ala Glu Lys
          195          200

```

```

<210> 91
<211> 188
<212> PRT
<213> Haemophilus influenzae

<220>
<221> PEPTIDE
<222> (47)
<223> X at position 47 is undefined

<220>
<221> PEPTIDE

```


Sequence_Listing_R10901_Corrected.txt

<222> {57}

<223> X at position 57 is undefined

<400> 91

Met Ile Asn Pro Asn Arg Gln Ile Val Leu Asp Thr Glu Thr Thr Gly
1 5 10 15

Met Asn Gln Leu Gly Ala His Tyr Glu Gly His Cys Ile Ile Glu Ile
20 25 30

Gly Ala Val Glu Leu Ile Asn Arg Arg Tyr Thr Gly Asn Asn Xaa His
35 40 45

Ile Tyr Ile Lys Pro Asp Arg Pro Xaa Asp Pro Asp Ala Ile Lys Val
50 55 60

His Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Pro Glu Phe Lys Glu
65 70 75 80

Val Ala Gln Asp Phe Leu Asp Tyr Ile Asn Gly Ala Glu Leu Leu Ile
85 90 95

His Asn Ala Pro Phe Asp Val Gly Phe Met Asp Tyr Glu Phe Arg Lys
100 105 110

Leu Asn Leu Asn Val Lys Thr Asp Asp Ile Cys Leu Val Thr Asp Thr
115 120 125

Leu Gln Met Ala Arg Gln Met Tyr Pro Gly Lys Arg Asn Asn Leu Asp
130 135 140

Ala Leu Cys Asp Arg Leu Gly Ile Asp Asn Ser Lys Arg Thr Leu His
145 150 155 160

Gly Ala Leu Leu Asp Ala Glu Ile Leu Ala Asp Val Tyr Leu Met Met
165 170 175

Thr Gly Gly Gln Thr Asn Leu Phe Asp Glu Glu Glu
180 185

<210> 92

<211> 189

<212> PRT

<213> Escherichia coli

<400> 92

Met Ser Thr Ala Ile Thr Arg Gln Ile Val Leu Asp Thr Glu Thr Thr
1 5 10 15

Gly Met Asn Gln Ile Gly Ala His Ser Glu Gly His Lys Ile Ile Glu
20 25 30

Ile Gly Ala Val Glu Val Val Asn Arg Arg Leu Thr Gly Asn Asn Phe
35 40 45

His Val Tyr Leu Lys Asp Arg Leu Val Asp Pro Glu Ala Phe Gly Val
50 55 60

Sequence_Listing_R10901_Corrected.txt

```

His Gly Ile Ala Val Asp Phe Leu Leu Asp Lys Pro Thr Phe Ala Glu
 65          70          75          80
Val Ala Val Glu Phe Met Asp Tyr Ile Arg Gly Ala Glu Leu Val Ile
          85          90          95
His Asn Ala Ala Phe Asp Ile Gly Phe Met Asp Tyr Glu Phe Ser Leu
          100          105          110
Leu Lys Arg Asp Ile Ala Lys Thr Asn Thr Phe Cys Lys Val Thr Asp
          115          120          125
Ser Leu Ala Val Ala Arg Lys Met Phe Pro Gly Lys Arg Asn Ser Leu
          130          135          140
Asp Ala Leu Cys Ala Arg Tyr Glu Ile Asp Asn Ser Lys Arg Thr Leu
          145          150          155          160
His Gly Ala Leu Leu Asp Ala Gln Ile Leu Ala Glu Val Tyr Leu Ala
          165          170          175
Met Thr Gly Gly Gln Thr Ser Met Ala Phe Ala Met Glu
          180          185

```

<210> 93

<211> 201

<212> PRT

<213> Helicobacter pylori

<400> 93

```

Asn Leu Glu Tyr Leu Lys Ala Cys Gly Leu Asn Phe Ile Glu Thr Ser
 1          5          10          15
Glu Asn Leu Ile Thr Leu Lys Asn Leu Lys Thr Pro Leu Lys Asp Glu
          20          25          30
Val Phe Ser Phe Ile Asp Leu Glu Thr Thr Gly Ser Cys Pro Ile Lys
          35          40          45
His Glu Ile Leu Glu Ile Gly Ala Val Gln Val Lys Gly Gly Glu Ile
          50          55          60
Ile Asn Arg Phe Glu Thr Leu Val Lys Val Lys Ser Val Pro Asp Tyr
          65          70          75          80
Ile Ala Glu Leu Thr Gly Ile Thr Tyr Glu Asp Thr Leu Asn Ala Pro
          85          90          95
Ser Ala His Glu Ala Leu Gln Glu Leu Arg Leu Phe Leu Gly Asn Ser
          100          105          110
Val Phe Val Ala His Asn Ala Asn Phe Asp Tyr Asn Phe Leu Gly Arg
          115          120          125
Tyr Phe Val Glu Lys Leu His Cys Pro Leu Leu Asn Leu Lys Leu Cys
          130          135          140
Thr Leu Asp Leu Ser Lys Arg Ala Ile Leu Ser Met Arg Tyr Ser Leu

```

Sequence_Listing_R10901_Corrected.txt

145 150 155 160

Ser Phe Leu Lys Glu Leu Leu Gly Phe Gly Ile Glu Val Ser His Arg
165 170 175

Ala Tyr Ala Asp Ala Leu Ala Ser Tyr Lys Leu Phe Glu Ile Cys Leu
180 185 190

Leu Asn Leu Pro Ser Tyr Ile Lys Thr
195 200

<210> 94

<211> 630

<212> DNA

<213> Thermus thermophilus

<400> 94

```
atgggtggagc ggggtggtgcg gacccttctg gacgggaggt tectcttgga ggaggggggtg 60
gggctttggg agtggcgcta ccccttccc ctggaggggg aggcggtggt ggtcctggac 120
ctggagacca cgggcttgc cggcctggac gaggtgatt aggtgggacct cctccgctg 180
gaggggggga ggccctccc ctccagagc ctgcctcggc cctcccgcc cgcgaagcc 240
cgttcgtgga acctcacgg catccccgg gaggccttg aggaggcccc ctccctggag 300
gaggttctgg agaaggcta cccctccgc ggcgacgcca cttggtgat ccacaacgcc 360
gcctttgacc tgggcttct ccgcccggc ttggagggcc tgggtacgg cctgaaaac 420
cccggtgtgg actccctgc ctggccaga cggggcttac caggccttag cgcctacgcc 480
ctggacgccc tctccgaggt cctggagctt cccgaagga cctgccacg ggccctcgag 540
gacgtggagc gcacctcgc cgtggtgac gaggtatact atatgcttac gtcgggcct 600
ccccgcacg tttgggaact cgggaggtag 630
```

<210> 95

<211> 210

<212> PRT

<213> Thermus thermophilus

<400> 95

```
Met Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu
  1                      5                      10                      15

Glu Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu
 20                      25                      30

Gly Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly
 35                      40                      45

Leu Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg
 50                      55                      60

Arg Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala
 65                      70                      75                      80

Arg Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala
 85                      90                      95

Pro Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp
100                      105                      110

Ala Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg
```

Sequence_Listing_R10901_Corrected.txt
120 125

115

Pro Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp
130 135 140
Ser Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly
145 150 155 160
Leu Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His
165 170 175
Arg Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val
180 185 190
Tyr Tyr Met Leu Thr Ser Gly Arg Pro Arg Thr Leu Trp Glu Leu Gly
195 200 205
Arg Glx
210

<210> 96
<211> 461
<212> PRT
<213> *Pseudomonas marcesans*

<400> 96
Met Leu Glu Ala Ser Trp Glu Lys Val Gln Ser Ser Leu Lys Gln Asn
1 5 10 15
Leu Ser Lys Pro Ser Tyr Glu Thr Trp Ile Arg Pro Thr Glu Phe Ser
20 25 30
Gly Phe Lys Asn Gly Glu Leu Thr Leu Ile Ala Pro Asn Ser Phe Ser
35 40 45
Ser Ala Trp Leu Lys Asn Asn Tyr Ser Gln Thr Ile Gln Glu Thr Ala
50 55 60
Glu Glu Ile Phe Gly Glu Pro Val Thr Val His Val Lys Val Lys Ala
65 70 75 80
Asn Ala Glu Ser Ser Asp Glu His Tyr Ser Ser Ala Pro Ile Thr Pro
85 90 95
Pro Leu Glu Ala Ser Pro Gly Ser Val Asp Ser Ser Gly Ser Ser Leu
100 105 110
Arg Leu Ser Lys Lys Thr Leu Pro Leu Leu Asn Leu Arg Tyr Val Phe
115 120 125
Asn Arg Phe Val Val Gly Pro Asn Ser Arg Met Ala His Ala Ala Ala
130 135 140
Met Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe Ile
145 150 155 160
Cys Gly Gly Val Gly Leu Gly Lys Thr His Leu Met Gln Ala Ile Gly
165 170 175

Sequence_Listing_R10901_Corrected.txt

```

His Tyr Arg Leu Glu Ile Asp Pro Gly Ala Lys Val Ser Tyr Val Ser
      180                               185                               190

Thr Glu Thr Phe Thr Asn Asp Leu Ile Leu Ala Ile Arg Gln Asp Arg
      195                               200                               205

Met Gln Ala Phe Arg Asp Arg Tyr Arg Ala Ala Asp Leu Ile Leu Val
      210                               215                               220

Asp Asp Ile Gln Phe Ile Glu Gly Lys Glu Tyr Thr Gln Glu Glu Phe
      225                               230                               235                               240

Phe His Thr Phe Asn Ala Leu His Asp Ala Gly Ser Gln Ile Val Leu
      245                               250                               255

Ala Ser Asp Arg Pro Pro Ser Gln Ile Pro Arg Leu Gln Glu Arg Leu
      260                               265                               270

Met Ser Arg Phe Ser Met Gly Leu Ile Ala Asp Val Gln Ala Pro Asp
      275                               280                               285

Leu Glu Thr Arg Met Ala Ile Leu Gln Lys Lys Ala Glu His Glu Arg
      290                               295                               300

Val Gly Leu Pro Arg Asp Leu Ile Gln Phe Ile Ala Gly Arg Phe Thr
      305                               310                               315                               320

Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Thr Arg Ala Ile Ala Phe
      325                               330                               335

Ala Ser Ile Thr Gly Leu Pro Met Thr Val Asp Ser Ile Ala Pro Met
      340                               345                               350

Leu Asp Pro Asn Gly Gln Gly Val Glu Val Thr Pro Lys Gln Val Leu
      355                               360                               365

Asp Lys Val Ala Glu Val Phe Lys Val Thr Pro Asp Glu Met Arg Ser
      370                               375                               380

Ala Ser Arg Arg Arg Pro Val Ser Gln Ala Arg Gln Val Gly Met Tyr
      385                               390                               395                               400

Leu Met Arg Gln Gly Thr Asn Leu Ser Leu Pro Arg Ile Gly Asp Thr
      405                               410                               415

Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ala Ile Glu Gln Val
      420                               425                               430

Glu Lys Lys Leu Ser Ser Asp Pro Gln Ile Ala Ser Gln Val Gln Lys
      435                               440                               445

Ile Arg Asp Leu Leu Gln Ile Asp Ser Arg Arg Lys Arg
      450                               455                               460

```

<210> 97
 <211> 447
 <212> PRT

<213> Synechocystis sp.

<400> 97

```

Met Val Ser Cys Glu Asn Leu Trp Gln Gln Ala Leu Ala Ile Leu Ala
 1           5           10           15

Thr Gln Leu Thr Lys Pro Ala Phe Asp Thr Trp Ile Lys Ala Ser Val
      20           25           30

Leu Ile Ser Leu Gly Asp Gly Val Ala Thr Ile Gln Val Glu Asn Gly
 35           40           45

Phe Val Leu Asn His Leu Gln Lys Ser Tyr Gly Pro Leu Leu Met Glu
 50           55           60

Val Leu Thr Asp Leu Thr Gly Gln Glu Ile Thr Val Lys Leu Ile Thr
 65           70           75           80

Asp Gly Leu Glu Pro His Ser Leu Ile Gly Gln Glu Ser Ser Leu Pro
      85           90           95

Met Glu Thr Thr Pro Lys Asn Ala Thr Ala Leu Asn Gly Lys Tyr Thr
      100           105           110

Phe Ser Arg Phe Val Val Gly Pro Thr Asn Arg Met Ala His Ala Ala
 115           120           125

Ser Leu Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe
 130           135           140

Leu Cys Gly Gly Val Gly Leu Gly Lys Thr His Leu Met Gln Ala Ile
 145           150           155           160

Ala His Tyr Arg Leu Glu Met Tyr Pro Asn Ala Lys Val Tyr Val
      165           170           175

Ser Thr Glu Arg Phe Thr Asn Asp Leu Ile Thr Ala Ile Arg Gln Asp
      180           185           190

Asn Met Glu Asp Phe Arg Ser Tyr Tyr Arg Ser Ala Asp Phe Leu Leu
      195           200           205

Ile Asp Asp Ile Gln Phe Ile Lys Gly Lys Glu Tyr Thr Gln Glu Glu
 210           215           220

Phe Phe His Thr Phe Asn Ser Leu His Glu Ala Gly Lys Gln Val Val
 225           230           235           240

Val Ala Ser Asp Arg Ala Pro Gln Arg Ile Pro Gly Leu Gln Asp Arg
      245           250           255

Leu Ile Ser Arg Phe Ser Met Gly Leu Ile Ala Asp Ile Gln Val Pro
      260           265           270

Asp Leu Glu Thr Arg Met Ala Ile Leu Gln Lys Lys Ala Glu Tyr Asp
      275           280           285

Arg Ile Arg Leu Pro Lys Glu Val Ile Glu Tyr Ile Ala Ser His Tyr
 290           295           300

```

Sequence_Listing_R10901_Corrected.txt

Thr Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Ala Ile Ala
305 310 315 320

Tyr Thr Ser Leu Ser Asn Val Ala Met Thr Val Glu Asn Ile Ala Pro
325 330 335

Val Leu Asn Pro Pro Val Glu Lys Val Ala Ala Ala Pro Glu Thr Ile
340 345 350

Ile Thr Ile Val Ala Gln His Tyr Gln Leu Lys Val Glu Glu Leu Leu
355 360 365

Ser Asn Ser Arg Arg Arg Glu Val Ser Leu Ala Arg Gln Val Gly Met
370 375 380

Tyr Leu Met Arg Gln His Thr Asp Leu Ser Leu Pro Arg Ile Gly Glu
385 390 395 400

Ala Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ser Cys Asp Lys
405 410 415

Ile Thr Gln Leu Gln Gln Lys Asp Trp Glu Thr Ser Gln Thr Leu Thr
420 425 430

Ser Leu Ser His Arg Ile Asn Ile Ala Gly Gln Ala Pro Glu Ser
435 440 445

<210> 98

<211> 446

<212> PRT

<213> *Bacillus subtilis*

<400> 98

Met Glu Asn Ile Leu Asp Leu Trp Asn Gln Ala Leu Ala Gln Ile Glu
1 5 10 15

Lys Lys Leu Ser Lys Pro Ser Phe Glu Thr Trp Met Lys Ser Thr Lys
20 25 30

Ala His Ser Leu Gln Gly Asp Thr Leu Thr Ile Thr Ala Pro Asn Glu
35 40 45

Phe Ala Arg Asp Trp Leu Glu Ser Arg Tyr Leu His Leu Ile Ala Asp
50 55 60

Thr Ile Tyr Glu Leu Thr Gly Glu Glu Leu Ser Ile Lys Phe Val Ile
65 70 75 80

Pro Gln Asn Gln Asp Val Glu Asp Phe Met Pro Lys Pro Gln Val Lys
85 90 95

Lys Ala Val Lys Glu Asp Thr Ser Asp Phe Pro Gln Asn Met Leu Asn
100 105 110

Pro Lys Tyr Thr Phe Asp Thr Phe Val Ile Gly Ser Gly Asn Arg Phe
115 120 125

Sequence Listing_R10901 Corrected.txt

Ala His Ala Ala Ser Leu Ala Val Ala Glu Ala Pro Ala Lys Ala Tyr
 130 135 140

Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr His Leu
 145 150 155 160

Met His Ala Ile Gly His Tyr Val Ile Asp His Asn Pro Ser Ala Lys
 165 170 175

Val Val Tyr Leu Ser Ser Glu Lys Phe Thr Asn Glu Phe Ile Asn Ser
 180 185 190

Ile Arg Asp Asn Lys Ala Val Asp Phe Arg Asn Arg Tyr Arg Asn Val
 195 200 205

Asp Val Leu Leu Ile Asp Asp Ile Gln Phe Leu Ala Gly Lys Glu Gln
 210 215 220

Thr Gln Glu Glu Phe Phe His Thr Phe Asn Thr Leu His Glu Glu Ser
 225 230 235 240

Lys Gln Ile Val Ile Ser Ser Asp Arg Pro Pro Lys Glu Ile Pro Thr
 245 250 255

Leu Glu Asp Arg Leu Arg Ser Arg Phe Glu Trp Gly Leu Ile Thr Asp
 260 265 270

Ile Thr Pro Pro Asp Leu Glu Thr Arg Ile Ala Ile Leu Arg Lys Lys
 275 280 285

Ala Lys Ala Glu Gly Leu Asp Ile Pro Asn Glu Val Met Leu Tyr Ile
 290 295 300

Ala Asn Gln Ile Asp Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile
 305 310 315 320

Arg Val Val Ala Tyr Ser Ser Leu Ile Asn Lys Asp Ile Asn Ala Asp
 325 330 335

Leu Ala Ala Glu Ala Leu Lys Asp Ile Ile Pro Ser Ser Lys Pro Lys
 340 345 350

Val Ile Thr Ile Lys Glu Ile Gln Arg Val Val Gly Gln Gln Phe Asn
 355 360 365

Ile Lys Leu Glu Asp Phe Lys Ala Lys Lys Arg Thr Lys Ser Val Ala
 370 375 380

Phe Pro Arg Gln Ile Ala Met Tyr Leu Ser Arg Glu Met Thr Asp Ser
 385 390 395 400

Ser Leu Pro Lys Ile Gly Glu Glu Phe Gly Gly Arg Asp His Thr Thr
 405 410 415

Val Ile His Ala His Glu Lys Ile Ser Lys Leu Leu Ala Asp Asp Glu
 420 425 430

Gln Leu Gln Gln His Val Lys Glu Ile Lys Glu Gln Leu Lys
 435 440 445

Sequence_Listing_R10901_Corrected.txt

<210> 99

<211> 507

<212> PRT

<213> Mycobacterium tuberculosis

<400> 99

Met Thr Asp Asp Pro Gly Ser Gly Phe Thr Thr Val Trp Asn Ala Val
1 5 10 15

Val Ser Glu Leu Asn Gly Asp Pro Lys Val Asp Asp Gly Pro Ser Ser
20 25 30

Asp Ala Asn Leu Ser Ala Pro Ile Thr Pro Gln Gln Arg Ala Trp Leu
35 40 45

Asn Leu Val Gln Pro Leu Thr Ile Val Glu Gly Phe Ala Leu Leu Ser
50 55 60

Val Pro Ser Ser Phe Val Gln Asn Glu Ile Glu Arg His Leu Arg Ala
65 70 75 80

Pro Ile Thr Asp Ala Leu Ser Arg Arg Leu Gly His Gln Ile Gln Leu
85 90 95

Gly Val Arg Ile Ala Pro Pro Ala Thr Asp Glu Ala Asp Asp Thr Thr
100 105 110

Val Pro Pro Ser Glu Asn Pro Ala Thr Thr Ser Pro Asp Thr Thr Thr
115 120 125

Asp Asn Asp Glu Ile Asp Asp Ser Ala Ala Ala Arg Gly Asp Asn Gln
130 135 140

His Ser Trp Pro Ser Tyr Phe Thr Glu Arg Pro His Asn Thr Asp Ser
145 150 155 160

Ala Thr Ala Gly Val Thr Ser Leu Asn Arg Arg Tyr Thr Phe Asp Thr
165 170 175

Phe Val Ile Gly Ala Ser Asn Arg Phe Ala His Ala Ala Ala Leu Ala
180 185 190

Ile Ala Glu Ala Pro Ala Arg Ala Tyr Asn Pro Leu Phe Ile Trp Gly
195 200 205

Glu Ser Gly Leu Gly Lys Thr His Leu Leu His Ala Ala Gly Asn Tyr
210 215 220

Ala Gln Arg Leu Phe Pro Gly Met Arg Val Lys Tyr Val Ser Thr Glu
225 230 235 240

Glu Phe Thr Asn Asp Phe Ile Asn Ser Leu Arg Asp Asp Arg Lys Val
245 250 255

Ala Phe Lys Arg Ser Tyr Arg Asp Val Asp Val Leu Leu Val Asp Asp
260 265 270

Sequence_Listing_R10901_Corrected.txt

```

Ile Gln Phe Ile Glu Gly Lys Glu Gly Ile Gln Glu Glu Phe Phe His
275                               280
Thr Phe Asn Thr Leu His Asn Ala Asn Lys Gln Ile Val Ile Ser Ser
290                               295                               300
Asp Arg Pro Pro Lys Gln Leu Ala Thr Leu Glu Asp Arg Leu Arg Thr
305                               310                               315                               320
Arg Phe Glu Trp Gly Leu Ile Thr Asp Val Gln Pro Pro Glu Leu Glu
325                               330                               335
Thr Arg Ile Ala Ile Leu Arg Lys Lys Ala Gln Met Glu Arg Leu Ala
340                               345                               350
Val Pro Asp Asp Val Leu Glu Leu Ile Ala Ser Ser Ile Glu Arg Asn
355                               360                               365
Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Val Thr Ala Phe Ala Ser
370                               375                               380
Leu Asn Lys Thr Pro Ile Asp Lys Ala Leu Ala Glu Ile Val Leu Arg
385                               390                               395                               400
Asp Leu Ile Ala Asp Ala Asn Thr Met Gln Ile Ser Ala Ala Thr Ile
405                               410                               415
Met Ala Ala Thr Ala Glu Tyr Phe Asp Thr Thr Val Glu Glu Leu Arg
420                               425                               430
Gly Pro Gly Lys Thr Arg Ala Leu Ala Gln Ser Arg Gln Ile Ala Met
435                               440                               445
Tyr Leu Cys Arg Glu Leu Thr Asp Leu Ser Leu Pro Lys Ile Gly Gln
450                               455                               460
Ala Phe Gly Arg Asp His Thr Thr Val Met Tyr Ala Gln Arg Lys Ile
465                               470                               475                               480
Leu Ser Glu Met Ala Glu Arg Arg Glu Val Phe Asp His Val Lys Glu
485                               490                               495
Leu Thr Thr Arg Ile Arg Gln Arg Ser Lys Arg
500                               505

<210> 100
<211> 446
<212> PRT
<213> Thermus thermophilus

<400> 100
Met Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
1                               5                               10                               15
Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
20                               25                               30
Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe

```

Sequence_Listing_R10901_Corrected.txt

```

35                               40                               45
Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly
 50                               55                               60
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val
 65                               70                               75                               80
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro
 85                               90                               95
Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly
100                               105                               110
Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser
115                               120                               125
Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu
130                               135                               140
Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg
145                               150                               155                               160
Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn
165                               170                               175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg
180                               185                               190
Glu Arg Tyr Arg Ser Val Asp Leu Leu Val Asp Asp Val Gln Phe
195                               200                               205
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn
210                               215                               220
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro
225                               230                               235                               240
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu
245                               250                               255
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile
260                               265                               270
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp
275                               280                               285
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp
290                               295                               300
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val
305                               310                               315                               320
Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro
325                               330                               335
Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly
340                               345                               350

```

Sequence Listing_R10901_Corrected.txt

Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys
355 360 365

Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu
370 375 380

Leu Thr Pro Ala Ser Leu Pro Glu Ile Gly Gln Leu Phe Gly Gly Arg
385 390 395 400

Asp His Thr Thr Val Arg Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala
405 410 415

Gly Lys Pro Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu
420 425 430

Ala Cys Thr Asp Pro Val Asp Asn Leu Trp Ile Thr Cys Gly
435 440 445

<210> 101

<211> 467

<212> PRT

<213> Escherichia coli

<400> 101

Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
1 5 10 15

Leu Pro Ala Thr Glu Phe Ser Met Trp Ile Arg Pro Leu Gln Ala Glu
20 25 30

Leu Ser Asp Asn Thr Leu Ala Leu Tyr Ala Pro Asn Arg Phe Val Leu
35 40 45

Asp Trp Val Arg Asp Lys Tyr Leu Asn Asn Ile Asn Gly Leu Leu Thr
50 55 60

Ser Phe Cys Gly Ala Asp Ala Pro Gln Leu Arg Phe Glu Val Gly Thr
65 70 75 80

Lys Pro Val Thr Gln Thr Pro Gln Ala Ala Val Thr Ser Asn Val Ala
85 90 95

Ala Pro Ala Gln Val Ala Gln Thr Gln Pro Gln Arg Ala Ala Pro Ser
100 105 110

Thr Arg Ser Gly Trp Asp Asn Val Pro Ala Pro Ala Glu Pro Thr Tyr
115 120 125

Arg Ser Asn Val Asn Val Lys His Thr Phe Asp Asn Phe Val Glu Gly
130 135 140

Lys Ser Asn Gln Leu Ala Arg Ala Ala Ala Arg Gln Val Ala Asp Asn
145 150 155 160

Pro Gly Gly Ala Tyr Asn Pro Leu Phe Leu Tyr Gly Gly Thr Gly Leu
165 170 175

Gly Lys Thr His Leu Leu His Ala Val Gly Asn Gly Ile Met Ala Arg

Sequence_Listing_R10901_Corrected.txt

```

180                               185                               190
Lys Pro Asn Ala Lys Val Val Tyr Met His Ser Glu Arg Phe Val Gln
195                               200                               205
Asp Met Val Lys Ala Leu Gln Asn Asn Ala Ile Glu Glu Phe Lys Arg
210                               215                               220
Tyr Tyr Arg Ser Val Asp Ala Leu Leu Ile Asp Asp Ile Gln Phe Phe
225                               230                               235                               240
Ala Asn Lys Glu Arg Ser Gln Glu Glu Phe Phe His Thr Phe Asn Ala
245                               250                               255
Leu Leu Glu Gly Asn Gln Gln Ile Ile Leu Thr Ser Asp Arg Tyr Pro
260                               265                               270
Lys Glu Ile Asn Gly Val Glu Asp Arg Leu Lys Ser Arg Phe Gly Trp
275                               280                               285
Gly Leu Thr Val Ala Ile Glu Pro Pro Glu Leu Glu Thr Arg Val Ala
290                               295                               300
Ile Leu Met Lys Lys Ala Asp Glu Asn Asp Ile Arg Leu Pro Gly Glu
305                               310                               315                               320
Val Ala Phe Phe Ile Ala Lys Arg Leu Arg Ser Asn Val Arg Glu Leu
325                               330                               335
Glu Gly Ala Leu Asn Arg Val Ile Ala Asn Ala Asn Phe Thr Gly Arg
340                               345                               350
Ala Ile Thr Ile Asp Phe Val Arg Glu Ala Leu Arg Asp Leu Leu Ala
355                               360                               365
Leu Gln Glu Lys Leu Val Thr Ile Asp Asn Ile Gln Lys Thr Val Ala
370                               375                               380
Glu Tyr Tyr Lys Ile Lys Val Ala Asp Leu Leu Ser Lys Arg Arg Ser
385                               390                               395                               400
Arg Ser Val Ala Arg Pro Arg Gln Met Ala Met Ala Leu Ala Lys Glu
405                               410                               415
Leu Thr Asn His Ser Leu Pro Glu Ile Gly Asp Ala Phe Gly Gly Arg
420                               425                               430
Asp His Thr Thr Val Leu His Ala Cys Arg Lys Ile Glu Gln Leu Arg
435                               440                               445
Glu Glu Ser His Asp Ile Lys Glu Asp Phe Ser Asn Leu Ile Arg Thr
450                               455                               460
Leu Ser Ser
465

```

<210> 102

<211> 440

Sequence_Listing_R10901_Corrected.txt

<212> PRT

<213> *Thermatoga maritima*

<400> 102

```

Met Lys Glu Arg Ile Leu Gln Glu Ile Lys Thr Arg Val Asn Arg Lys
 1           5           10           15

Ser Trp Glu Leu Trp Phe Ser Ser Phe Asp Val Lys Ser Ile Glu Gly
      20           25           30

Asn Lys Val Val Phe Ser Val Gly Asn Leu Phe Ile Lys Glu Trp Leu
      35           40           45

Glu Lys Lys Tyr Tyr Ser Val Leu Ser Lys Ala Val Lys Val Val Leu
      50           55           60

Gly Asn Asp Ala Thr Phe Glu Ile Thr Tyr Glu Ala Phe Glu Pro His
      65           70           75           80

Ser Ser Tyr Ser Glu Pro Leu Val Lys Lys Arg Ala Val Leu Leu Thr
      85           90           95

Pro Leu Asn Pro Asp Tyr Thr Phe Glu Asn Phe Val Val Gly Pro Gly
      100          105          110

Asn Ser Phe Ala Tyr His Ala Ala Leu Glu Val Ala Lys His Pro Gly
      115          120          125

Arg Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr
      130          135          140

His Leu Leu Gln Ser Ile Gly Asn Tyr Val Val Gln Asn Glu Pro Asp
      145          150          155          160

Leu Arg Val Met Tyr Ile Thr Ser Glu Lys Phe Leu Asn Asp Leu Val
      165          170          175

Asp Ser Met Lys Glu Gly Lys Leu Asn Glu Phe Arg Glu Lys Tyr Arg
      180          185          190

Lys Lys Val Asp Ile Leu Leu Ile Asp Asp Val Gln Phe Leu Ile Gly
      195          200          205

Lys Thr Gly Val Gln Thr Glu Leu Phe His Thr Phe Asn Glu Leu His
      210          215          220

Asp Ser Gly Lys Gln Ile Val Ile Cys Ser Asp Arg Glu Pro Gln Lys
      225          230          235          240

Leu Ser Glu Phe Gln Asp Arg Leu Val Ser Arg Phe Gln Met Gly Leu
      245          250          255

Val Ala Lys Leu Glu Pro Pro Asp Glu Glu Thr Arg Lys Ser Ile Ala
      260          265          270

Arg Lys Met Leu Glu Ile Glu His Gly Glu Leu Pro Glu Glu Val Leu
      275          280          285

Asn Phe Val Ala Glu Asn Val Asp Asp Asn Leu Arg Arg Leu Arg Gly

```

Sequence_Listing_R10901_Corrected.txt

290

295

300

Ala Ile Ile Lys Leu Leu Val Tyr Lys Glu Thr Thr Gly Lys Glu Val
 305 310 315 320

Asp Leu Lys Glu Ala Ile Leu Leu Leu Lys Asp Phe Ile Lys Pro Asn
 325 330 335

Arg Val Lys Ala Met Asp Pro Ile Asp Glu Leu Ile Glu Ile Val Ala
 340 345 350

Lys Val Thr Gly Val Pro Arg Glu Glu Ile Leu Ser Asn Ser Arg Asn
 355 360 365

Val Lys Ala Leu Thr Ala Arg Arg Ile Gly Met Tyr Val Ala Lys Asn
 370 375 380

Tyr Leu Lys Ser Ser Leu Arg Thr Ile Ala Glu Lys Phe Asn Arg Ser
 385 390 395 400

His Pro Val Val Val Asp Ser Val Lys Lys Val Lys Asp Ser Leu Leu
 405 410 415

Lys Gly Asn Lys Gln Leu Lys Ala Leu Ile Asp Glu Val Ile Gly Glu
 420 425 430

Ile Ser Arg Arg Ala Leu Ser Gly
 435 440

<210> 103

<211> 457

<212> PRT

<213> Helicobacter pylori

<400> 103

Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys
 1 5 10 15

Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln
 20 25 30

Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr
 35 40 45

Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala
 50 55 60

Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala
 65 70 75 80

His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn
 85 90 95

Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp
 100 105 110

Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val
 115 120 125

Sequence_Listing_R10901_Corrected.txt

```

Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn
130 135 140
Pro Val Leu Phe Tyr Gly Gly Thr Gly Leu Gly Lys Thr His Ile Leu
145 150 155 160
Asn Ala Ile Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu
165 170 175
Val Thr Ser Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn
180 185 190
Lys Thr Met Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe
195 200 205
Leu Leu Asp Asp Ala Gln Phe Leu Gln Gly Lys Pro Lys Leu Glu Glu
210 215 220
Glu Phe Phe His Thr Phe Asn Glu Leu His Ala Asn Ser Lys Gln Ile
225 230 235 240
Val Leu Ile Ser Asp Arg Ser Pro Lys Asn Ile Ala Gly Leu Glu Asp
245 250 255
Arg Leu Lys Ser Arg Phe Glu Trp Gly Ile Thr Ala Lys Val Met Pro
260 265 270
Pro Asp Leu Glu Thr Lys Leu Ser Ile Val Lys Gln Lys Cys Gln Leu
275 280 285
Asn Gln Ile Thr Leu Pro Glu Glu Val Met Glu Tyr Ile Ala Gln His
290 295 300
Ile Ser Asp Asn Ile Arg Gln Met Glu Gly Ala Ile Ile Lys Ile Ser
305 310 315 320
Val Asn Ala Asn Leu Met Asn Ala Ser Ile Asp Leu Asn Leu Ala Lys
325 330 335
Thr Val Leu Glu Asp Leu Gln Lys Asp His Ala Glu Gly Ser Ser Leu
340 345 350
Glu Asn Ile Leu Leu Ala Val Ala Gln Ser Leu Asn Leu Lys Ser Ser
355 360 365
Glu Ile Lys Val Ser Ser Arg Gln Lys Asn Val Ala Leu Ala Arg Lys
370 375 380
Leu Val Val Tyr Phe Ala Arg Leu Tyr Thr Pro Asn Pro Thr Leu Ser
385 390 395 400
Leu Ala Gln Phe Leu Asp Leu Lys Asp His Ser Ser Ile Ser Lys Met
405 410 415
Tyr Ser Gly Val Lys Lys Met Leu Glu Glu Glu Lys Ser Pro Phe Val
420 425 430
Leu Ser Leu Arg Glu Glu Ile Lys Asn Arg Leu Asn Glu Leu Asn Asp

```


Sequence_Listing_R10901_Corrected.txt

435

440

445

Lys Lys Thr Ala Phe Asn Ser Ser Glu

450

455

<210> 104

<211> 1305

<212> DNA

<213> *Thermus thermophilus*

<400> 104

```

gtgtgcacag aggcctgtctg gcaacacgtt ctggagcaca tccgcgcgag catcacccag 60
gtggagttcc acacctgtgtt tgaaggagtc cgcctcttgg ggatccggga cggggtgctg 120
gagctgcgag tgcccacctc ctttgccttg gactggatcc ggcgccacta ccgcggccto 180
atccaggagg gccctcggtt cctcgggggc caggcgcgcc ggtttgagct ccgggtgggt 240
cccggggtcg tagtccagga ggacatcttc cagcccccgc cgagccccc ggcccaagct 300
caaccogaag ataccttta aacttgttgg tggggcccaa caactccatg gccccaacgc 360
ggcgcgctgg ccgtggcgga gtcccccggc cgggcctaca acccctctt catctacggg 420
ggcgtgtggc tgggaaagac ctacctgatg cagcgcgtgg gccactccg tgcgaagcgc 480
ttccccaca tgagattaga gtacgtttcc acggaacct tcaccaacga gctcatcaac 540
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ctgctgttgg acgacgtcca gtctatcgcc ggaaggagc gcacccagga ggagttttc 660
cacaccttca acgcccctta cgaggcccac aagcagatca tctctcttc cgacggcgcc 720
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gagctgaccg gcgcctgtgg ggccaaggct ctccgacatc ttgcgccag ggagctggag 1020
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ggagctcagc gggagcgccg caagaaggag gtggtctct ccggcgagct acactgtac 1140
ctggtgcggg agctcaccoc ggctcctcgc cccagatcg accagctcaa cgacgacgg 1200
gaccacacca cgtctcctca cgccatccag aaggtccagg agctcgcgga aagcgacgg 1260
gaggtgcagg gcctctccg caccctccg gagcggtgca catga 1305

```

<210> 105

<211> 434

<212> PRT

<213> *Thermus thermophilus*

<400> 105

```

Val Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
  1           5           10          15
Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
  20          25          30
Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
  35          40          45
Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly
  50          55          60
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val
  65          70          75          80
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro
  85          90          95

```

Sequence_Listing_R10901_Corrected.txt

```

Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly
    100                                105                                110

Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser
    115                                120                                125

Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu
    130                                135                                140

Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg
    145                                150                                155                                160

Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn
    165                                170                                175

Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg
    180                                185                                190

Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe
    195                                200                                205

Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn
    210                                215                                220

Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro
    225                                230                                235                                240

Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu
    245                                250                                255

Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile
    260                                265                                270

Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp
    275                                280                                285

Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp
    290                                295                                300

Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val
    305                                310                                315                                320

Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro
    325                                330                                335

Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly
    340                                345                                350

Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys
    355                                360                                365

Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu
    370                                375                                380

Leu Thr Pro Ala Ser Leu Pro Glu Ile Asp Gln Leu Asn Asp Asp Arg
    385                                390                                395                                400

Asp His Thr Thr Val Leu Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala

```

Sequence_Listing_R10901_Corrected.txt

405

410

415

Glu Ser Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu Ala
 420 425 430

Cys Thr

<210> 106

<211> 1128

<212> DNA

<213> *Thermus thermophilus*

<400> 106

```

atgaacataa cggttcccaa aaaactcttc tcggaccagc ttccctctct ggagcgcata 60
gtccctctta gaagcgccaa cccctctctac acctacctgg ggctttacgc cgaggaaggg 120
gccttgatcc tcttcgggac caacggggag gtggacctcg aggtccgcct ccccgccgag 180
gcccagaagcc ttccccgggt gctcgtcccc gccagccctt tcttcagctt ggtgcggagc 240
cttctcgggg acctcgtggc cctcggcctc gcctcggagc cgggccaggg ggggcagctg 300
gagctctctc ccgggcgttt ccgcaccogg ctacgccttg cccctgcgga gggctacccc 360
gagcttctgg tgcccagagg ggaggacaag ggggccttcc cctccggac cgggatcccc 420
tcgggggagc tcgtcaaggg ctgaccacac gtgcgctacg ccgcgagcaa cgaggagtag 480
cgggccatct tcgcgggggt gcagctggag ttctccccc agggcttccg ggcggtggcc 540
tcgcaggggt acgcctcgc cctctacgac ctgcccctgc ccaaggggtt ccaggccaa 600
gccgtggttc ccgcccggag cgtggacgag atggtgcggg tctgaaggg ggcggacggg 660
gccgaggccg tctctgcctt gggcgagggg gtgttgccc tggcctcga ggcgggaagc 720
ggggcccgga tggccctcgc cctcatggaa ggggagttcc ccgactacca gagggtcact 780
ccccaggagt tcgcctcaa ggtccagggt gagggggagg cctcaggga ggcggtgcgc 840
cgggtgagcg tctctcga ccggcagaac caccgggtgg acctcctttt ggaggaagcg 900
cggatcctcc tctccgcga gggggaactac ggcaaggggc aggagggagt gcccgccag 960
gtggaggggc cggacatggc cgtggcctac aacgccgcct acctcctcga ggcctcgc 1020
ccggtggggg accgggcccc cctgggcctc tcggggccca cgagcccgag cctcatctg 1080
ggggcagggg aggggtacgc ggcggtggtg gtgcccctca ggtctatg 1128

```

<210> 107

<211> 376

<212> PRT

<213> *Thermus thermophilus*

<400> 107

```

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
  1 5 10 15
Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
  20 25 30
Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
  35 40 45
Gly Gly Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
  50 55 60
Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
  65 70 75 80
Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
  85 90 95

```

Sequence_Listing_R10901_Corrected.txt

```

Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
      100                      105                      110

Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
      115                      120                      125

Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
      130                      135                      140

Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
      145                      150                      155                      160

Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
      165                      170                      175

Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
      180                      185                      190

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
      195                      200                      205

Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
      210                      215                      220

Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
      225                      230                      235                      240

Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
      245                      250                      255

Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
      260                      265                      270

Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
      275                      280                      285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
      290                      295                      300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
      305                      310                      315                      320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
      325                      330                      335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
      340                      345                      350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
      355                      360                      365

Val Val Val Pro Leu Arg Val Glx
      370                      375

```

<210> 108

<211> 376

<212> PRT

Sequence_Listing_R10901_Corrected.txt

<213> Thermus thermophilus

<400> 108

```

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
 1           5           10           15

Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
          20           25           30

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
 35           40           45

Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
 50           55           60

Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
 65           70           75           80

Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
 85           90           95

Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
100           105           110

Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
115           120           125

Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
130           135           140

Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
145           150           155           160

Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
165           170           175

Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
180           185           190

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
195           200           205

Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
210           215           220

Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
225           230           235           240

Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
245           250           255

Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
260           265           270

Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
275           280           285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
290           295           300

```

Sequence_Listing_R10901_Corrected.txt

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Val Pro Ala Gln
305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
355 360 365

Val Val Val Pro Leu Arg Val Glx
370 375

<210> 109

<211> 367

<212> PRT

<213> Escherichia coli

<400> 109

Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln
1 5 10 15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
20 25 30

Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp
35 40 45

Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu
50 55 60

Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg
65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg
85 90 95

Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
100 105 110

Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe
115 120 125

Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe
130 135 140

Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe
145 150 155 160

Glu Thr Glu Gly Glu Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg
165 170 175

Leu Ala Val Cys Ser Met Pro Ile Gly Gln Ser Leu Pro Ser His Ser
180 185 190

Sequence_Listing_R10901_Corrected.txt

```

Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Met Leu Asp
 195                200                205

Gly Gly Asp Asn Pro Leu Arg Val Gln Ile Gly Ser Asn Asn Ile Arg
 210                215                220

Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly Arg
 225                230                235                240

Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Asp Lys His Leu
 245                250                255

Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala Phe Ala Arg Ala Ala Ile
 260                265                270

Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Leu Tyr Val Ser Glu Asn
 275                280                285

Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu Glu
 290                295                300

Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu Met Glu Ile Gly Phe Asn
 305                310                315                320

Val Ser Tyr Val Leu Asp Val Leu Asn Ala Leu Lys Cys Glu Asn Val
 325                330                335

Arg Met Met Leu Thr Asp Ser Val Ser Ser Val Gln Ile Glu Asp Ala
 340                345                350

Ala Ser Gln Ser Ala Ala Tyr Val Val Met Pro Met Arg Leu Glx
 355                360                365

```

<210> 110

<211> 367

<212> PRT

<213> Proteus mirabilis

<400> 110

```

Met Lys Phe Ile Ile Glu Arg Glu Gln Leu Leu Lys Pro Leu Gln Gln
 1                5                10                15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
 20                25                30

Leu Leu Leu Lys Val Thr Glu Asn Thr Leu Ser Leu Thr Gly Thr Asp
 35                40                45

Leu Glu Met Glu Met Met Ala Arg Val Ser Leu Ser Gln Ser His Glu
 50                55                60

Ile Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Trp Arg
 65                70                75                80

Gly Leu Pro Glu Gly Ala Glu Ile Ser Val Glu Leu Asp Gly Asp Arg
 85                90                95

Leu Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro

```

Sequence_Listing_R10901_Corrected.txt

```

100                               105                               110
Ala Ser Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe
115                               120                               125
Thr Leu Pro Gln Ala Thr Leu Lys Arg Leu Ile Glu Ser Thr Gln Phe
130                               135                               140
Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe
145                               150                               155                               160
Glu Thr Glu Asn Thr Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg
165                               170                               175
Leu Ala Val Cys Ala Met Asp Ile Gly Gln Ser Leu Pro Gly His Ser
180                               185                               190
Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Leu Leu Asp
195                               200                               205
Gly Ser Gly Glu Ser Leu Leu Gln Leu Gln Ile Gly Ser Asn Asn Leu
210                               215                               220
Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly
225                               230                               235                               240
Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Thr Lys Thr
245                               250                               255
Val Ile Ala Gly Cys Asp Ile Leu Lys Gln Ala Phe Ser Arg Ala Ala
260                               265                               270
Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Ile Asn Leu Thr Asn
275                               280                               285
Gly Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu
290                               295                               300
Glu Ile Val Asp Val Gln Tyr Gln Gly Glu Glu Met Glu Ile Gly Phe
305                               310                               315
Asn Val Ser Tyr Leu Leu Asp Val Leu Asn Thr Leu Lys Cys Glu Glu
325                               330                               335
Val Lys Leu Leu Leu Thr Asp Ala Val Ser Ser Val Gln Val Glu Asn
340                               345                               350
Val Ala Ser Ala Ala Ala Tyr Val Val Met Pro Met Arg Leu
355                               360                               365

```

<210> 111

<211> 366

<212> PRT

<213> Haemophilus influenzae

<400> 111

```

Met Gln Phe Ser Ile Ser Arg Glu Asn Leu Leu Lys Pro Leu Gln Gln
1                               5                               10                               15

```


Sequence_Listing_R10901_Corrected.txt

Val Cys Gly Val Leu Ser Asn Arg Pro Asn Ile Pro Val Leu Asn Asn
 20 25 30
 Val Leu Leu Gln Ile Glu Asp Tyr Arg Leu Thr Ile Thr Gly Thr Asp
 35 40 45
 Leu Glu Val Glu Leu Ser Ser Gln Thr Gln Leu Ser Ser Ser Glu
 50 55 60
 Asn Gly Thr Phe Thr Ile Pro Ala Lys Lys Phe Leu Asp Ile Cys Arg
 65 70 75 80
 Thr Leu Ser Asp Asp Ser Glu Ile Thr Val Thr Phe Glu Gln Asp Arg
 85 90 95
 Ala Leu Val Gln Ser Gly Arg Ser Arg Phe Thr Leu Ala Thr Gln Pro
 100 105 110
 Ala Glu Glu Tyr Pro Asn Leu Thr Asp Trp Gln Ser Glu Val Asp Phe
 115 120 125
 Glu Leu Pro Gln Asn Thr Leu Arg Arg Leu Ile Glu Ala Thr Gln Phe
 130 135 140
 Ser Met Ala Asn Gln Asp Ala Arg Tyr Phe Leu Asn Gly Met Lys Phe
 145 150 155 160
 Glu Thr Glu Gly Asn Leu Leu Arg Thr Val Ala Thr Asp Gly His Arg
 165 170 175
 Leu Ala Val Cys Thr Ile Ser Leu Glu Gln Glu Leu Gln Asn His Ser
 180 185 190
 Val Ile Leu Pro Arg Lys Gly Val Leu Glu Leu Val Arg Leu Leu Glu
 195 200 205
 Thr Asn Asp Glu Pro Ala Arg Leu Gln Ile Gly Thr Asn Asn Leu Arg
 210 215 220
 Val His Leu Lys Asn Thr Val Phe Thr Ser Lys Leu Ile Asp Gly Arg
 225 230 235 240
 Phe Pro Asp Tyr Arg Arg Val Leu Pro Arg Asn Ala Thr Lys Ile Val
 245 250 255
 Glu Gly Asn Trp Glu Met Leu Lys Gln Ala Phe Ala Arg Ala Ser Ile
 260 265 270
 Leu Ser Asn Glu Arg Ala Arg Ser Val Arg Leu Ser Leu Lys Glu Asn
 275 280 285
 Gln Leu Lys Ile Thr Ala Ser Asn Thr Glu His Glu Glu Ala Glu Glu
 290 295 300
 Ile Val Asp Val Asn Tyr Asn Gly Glu Glu Leu Glu Val Gly Phe Asn
 305 310 315 320
 Val Thr Tyr Ile Leu Asp Val Leu Asn Ala Leu Lys Cys Asn Gln Val

Sequence_Listing_R10901_Corrected.txt

325

330

335

Arg Met Cys Leu Thr Asp Ala Phe Ser Ser Cys Leu Ile Glu Asn Cys
 340 345 350

Glu Asp Ser Ser Cys Glu Tyr Val Ile Met Pro Met Arg Leu
 355 360 365

<210> 112

<211> 367

<212> PRT

<213> *Pseudomonas putida*

<400> 112

Met His Phe Thr Ile Gln Arg Glu Ala Leu Leu Lys Pro Leu Gln Leu
 1 5 10 15

Val Ala Gly Val Val Glu Arg Arg Gln Thr Leu Pro Val Leu Ser Asn
 20 25 30

Val Leu Leu Val Val Gln Gly Gln Gln Leu Ser Leu Thr Gly Thr Asp
 35 40 45

Leu Glu Val Glu Leu Val Gly Arg Val Gln Leu Glu Glu Pro Ala Glu
 50 55 60

Pro Gly Glu Ile Thr Val Pro Ala Arg Lys Leu Met Asp Ile Cys Lys
 65 70 75 80

Ser Leu Pro Asn Asp Ala Leu Ile Asp Ile Lys Val Asp Glu Gln Lys
 85 90 95

Leu Leu Val Lys Ala Gly Arg Ser Arg Phe Thr Leu Ser Thr Leu Pro
 100 105 110

Ala Asn Asp Phe Pro Thr Val Glu Glu Gly Pro Gly Ser Leu Thr Cys
 115 120 125

Asn Leu Glu Gln Ser Lys Leu Arg Arg Leu Ile Glu Arg Thr Ser Phe
 130 135 140

Ala Met Ala Gln Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
 145 150 155 160

Glu Val Ser Arg Asn Thr Leu Arg Ala Val Ser Thr Asp Gly His Arg
 165 170 175

Leu Ala Leu Cys Ser Met Ser Ala Pro Ile Glu Gln Glu Asp Arg His
 180 185 190

Gln Val Ile Val Pro Arg Lys Gly Ile Leu Glu Leu Ala Arg Leu Leu
 195 200 205

Thr Asp Pro Glu Gly Met Val Ser Ile Val Leu Gly Gln His His Ile
 210 215 220

Arg Ala Thr Thr Gly Glu Phe Thr Phe Thr Ser Lys Leu Val Asp Gly
 225 230 235 240

Sequence_Listing_R10901_Corrected.txt

Lys Phe Pro Asp Tyr Glu Arg Val Leu Pro Lys Gly Gly Asp Lys Leu
245 250 255
Val Val Gly Asp Arg Gln Ala Leu Arg Glu Ala Phe Ser Arg Thr Ala
260 265 270
Ile Leu Ser Asn Glu Lys Tyr Arg Gly Ile Arg Leu Gln Leu Ala Ala
275 280 285
Gly Gln Leu Lys Ile Gln Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu
290 295 300
Glu Glu Ile Ser Val Asp Tyr Glu Gly Ser Ser Leu Glu Ile Gly Phe
305 310 315 320
Asn Val Ser Tyr Leu Leu Asp Val Leu Gly Val Met Thr Thr Glu Gln
325 330 335
Val Arg Leu Ile Leu Ser Asp Ser Asn Ser Ser Ala Leu Leu Gln Glu
340 345 350
Ala Gly Asn Asp Asp Ser Ser Tyr Val Val Met Pro Met Arg Leu
355 360 365

<210> 113

<211> 366

<212> FRT

<213> Buchnera aphidicola

<400> 113

Met Lys Phe Thr Ile Gln Asn Asp Ile Leu Thr Lys Asn Leu Lys Lys
1 5 10 15
Ile Thr Arg Val Leu Val Lys Asn Ile Ser Phe Pro Ile Leu Glu Asn
20 25 30
Ile Leu Ile Gln Val Glu Asp Gly Thr Leu Ser Leu Thr Thr Asn
35 40 45
Leu Glu Ile Glu Leu Ile Ser Lys Ile Glu Ile Ile Thr Lys Tyr Ile
50 55 60
Pro Gly Lys Thr Thr Ile Ser Gly Arg Lys Ile Leu Asn Ile Cys Arg
65 70 75 80
Thr Leu Ser Glu Lys Ser Lys Ile Lys Met Gln Leu Lys Asn Lys Lys
85 90 95
Met Tyr Ile Ser Ser Glu Asn Ser Asn Tyr Ile Leu Ser Thr Leu Ser
100 105 110
Ala Asp Thr Phe Pro Asn His Gln Asn Phe Asp Tyr Ile Ser Lys Phe
115 120 125
Asp Ile Ser Ser Asn Ile Leu Lys Glu Met Ile Glu Lys Thr Glu Phe
130 135 140

Sequence_Listing_R10901_Corrected.txt

```

Ser Met Gly Lys Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
145          150          155          160

Glu Lys Lys Asp Lys Phe Leu Arg Ser Val Ala Thr Asp Gly Tyr Arg
          165          170          175

Leu Ala Ile Ser Tyr Thr Gln Leu Lys Lys Asp Ile Asn Phe Phe Ser
          180          185          190

Ile Ile Ile Pro Asn Lys Ala Val Met Glu Leu Leu Lys Leu Leu Asn
195          200          205

Thr Gln Pro Gln Leu Leu Asn Ile Leu Ile Gly Ser Asn Ser Ile Arg
210          215          220

Ile Tyr Thr Lys Asn Leu Ile Phe Thr Thr Gln Leu Ile Glu Gly Glu
225          230          235          240

Tyr Pro Asp Tyr Lys Ser Val Leu Phe Lys Lys Lys Asn Pro Ile
          245          250          255

Ile Thr Asn Ser Ile Leu Leu Lys Lys Ser Leu Leu Arg Val Ala Ile
260          265          270

Leu Ala His Glu Lys Phe Cys Gly Ile Glu Ile Lys Ile Glu Asn Gly
275          280          285

Lys Phe Lys Val Leu Ser Asp Asn Gln Glu Glu Glu Thr Ala Glu Asp
290          295          300

Leu Phe Glu Ile Asp Tyr Phe Gly Glu Lys Ile Glu Ile Ser Ile Asn
305          310          315          320

Val Tyr Tyr Leu Leu Asp Val Ile Asn Asn Ile Lys Ser Glu Asn Ile
325          330          335

Ala Leu Phe Leu Asn Lys Ser Lys Ser Ser Ile Gln Ile Glu Ala Glu
340          345          350

Asn Asn Ser Ser Asn Ala Tyr Val Val Met Leu Leu Lys Arg
355          360          365

```

<210> 114

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 114

gtgtggatcc tcgtcccccct catgcgcgcac caggaaggg

39

<210> 115

<211> 27

<212> DNA

<213> Artificial Sequence

Sequence_Listing_R10901_Corrected.txt

<220>

<223> Description of Artificial Sequence: primer

<400> 115

gtgtggtatcc gtgtgtgaacct tagccac

27

<210> 116

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 116

ttcgtgtccg aggcacctgt ggtccacaaac

30

<210> 117

<211> 3514

<212> DNA

<213> Aquifex aeolicus

<400> 117

atgagtaagg atttctgtcca ccttcacctg cacacccagt tctcactcct ggaacggggt 60
ataaagatag acgagctcgt gaaaaaggca aaggagtatg gatacaaaagc tgcgggaatg 120
tcagaccacg gaacacctctt cggttcgtat aaattctaca aagccctgaa ggcgggaagga 180
attaagccca taatcggtat ggaagccctac ttaccacagc gttcggaggtt tgacagaaag 240
actaaaaaga gcgaggacaa cataaccgac aagtacaacc accacctcat acttatagca 300
aaggacgaaa aggtctaaag aacttaatga agctctcaac cctcgccctac aaagaaggtt 360
tttactaaaa acccagaatt gattacgaac tcttgaaaa gtacggggag ggcctaatag 420
cccttaccgc atgcctgaaa ggtgttccca cctactacgc ttctataaac gaagtgtaaa 480
aggcggagga atgggttaag aagtccaagg atatactcg agatgaacct tatttagaac 540
ttcaagcgaa caacattcca gaacaggaaag tggcaaacag gaacttaata gagatagcca 600
aaaagtacga tgtgaaactc atagcgacgc aggcgcgcca ctacctcaat cccgaagaca 660
ggtagcgcca caccggtctt atggcacttc aaatgaaaaa gaccattcac gaactgagtt 720
cgggaaactt caagtgttca aacgaagacc ttcactttgc tccaccogag tacatgtgga 780
aaaagtttga aggttaagt cgaaggtcgg aaaaaggcact cctgaacact ctcgaggtaa 840
tggaanaagc agcgacagc tttgagatat ttgaaaactc cacttacctc ctccccaggt 900
acgacgttcc gcccgacaaa acccttgagg aatacctcag agaactcgcg tacaaaaggtt 960
taagacagag gatagaaaag ggacaagcta aggatactaa agagtactcg gagaggtctg 1020
agtacgaact ggaagtata aacaaaaatg gctttgcggg atactctctg atagttcagg 1080
acttcataaa ctgggctatg aaaaacgaca taccctgttg acccggaagg ggaagtctgt 1140
gaggttccct cgtcgcatc gccatcgga taacggacgt tgacctata taagcaggtat 1200
tcttttttga gaggtttctt aaccocgaaa gggtttccat gccggtata gacgtggagt 1260
tctgtcagga caacagggaa aggtctatag agtacgttaag gaacaagtlac ggacaagaca 1320
acgtagctca gataatcacc tacaacgtta tgaaggcgaa gcaaacactg agagacgtcg 1380
caaggccact gggaactccc tactccaccg cggacaaact cgcaaaaact attctctagg 1440
gggacgttca ggggaactgg ctacgtctgg aagagatgta caaaaacgct gtggagggaac 1500
tccttcagaa gtacggagaa cacagaacgg acatagagga caacgtaaaag aagttcagac 1560
agatatcgga agaaagtcgg gagataaaac agctcgttga gacggccctg aagcttgaag 1620
gtctacagag acacacctcc ctccacgccc cgggagtggt tatagcacca aagcccttga 1680
gcgagctcgt tcccctctac tacgataaag agggcgaaat gcacacccag tacgacatgg 1740
ttcagctcga agaactcgtt ctctctgaaga tggacttctc cggactcaaa accctcacag 1800
aactgaactc catgaagaa ctcatataag aaagacacgg agtggatata aacttctctg 1860
aacttccctt tgacgacccc aaagtttaca aactccttca ggaagggaaa accacgggag 1920
tgttccagct cgaagaagcagg ggaatgaaag aactcctgaa gaaactaaag cccgacagct 1980

Sequence_Listing_R10901_Corrected.txt

```

ttgacgacat cgttgcggctc ctcgcactct acagaccggg accctctaaa agcggactcg 2040
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tgtctcagat accttccggcg ttactcccg gagaggcgga taccctcaga aaggcgatag 2220
gtaaagaagaa agcggatttta atggctcaga tgaaagacaa gttcctacag ggaagcggtg 2280
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gccttgccga aaaactaaag ggaattattg aaaaacaacg gacggaggag ggatacaact 3300
tggttctcac ggttgatctg ggagactact tcgttgattt agcactccca caagatatga 3360
aactaaaggc tgacagaaga gtgttagagg agatagaaaa actgggagtg aaggtcataa 3420
tttagtaaat aacccttact tccgagtagt cccc 3514

```

<210> 118

<211> 1161

<212> PRT

<213> Aquifex aeolicus

<400> 118

```

Met Ser Lys Asp Phe Val His Leu His Leu His Thr Gln Phe Ser Leu
  1             5             10             15

```

```

Leu Asp Gly Ala Ile Lys Ile Asp Glu Leu Val Lys Lys Ala Lys Glu
      20             25             30

```

```

Tyr Gly Tyr Lys Ala Val Gly Met Ser Asp His Gly Asn Leu Phe Gly
  35             40             45

```

```

Ser Tyr Lys Phe Tyr Lys Ala Leu Lys Ala Glu Gly Ile Lys Pro Ile
  50             55             60

```

```

Ile Gly Met Glu Ala Tyr Phe Thr Thr Gly Ser Arg Phe Asp Arg Lys
  65             70             75             80

```

```

Thr Lys Thr Ser Glu Asp Asn Ile Thr Asp Lys Tyr Asn His His Leu
  85             90             95

```

```

Ile Leu Ile Ala Lys Asp Asp Lys Gly Leu Lys Asn Leu Met Lys Leu
  100            105            110

```

```

Ser Thr Leu Ala Tyr Lys Glu Gly Phe Tyr Tyr Lys Pro Arg Ile Asp
  115            120            125

```

```

Tyr Glu Leu Leu Glu Lys Tyr Gly Glu Gly Leu Ile Ala Leu Thr Ala

```

Sequence_Listing_R10901_Corrected.txt

```

130                               135                               140
Cys Leu Lys Gly Val Pro Thr Tyr Tyr Ala Ser Ile Asn Glu Val Lys
145                               150                               155                               160
Lys Ala Glu Glu Trp Val Lys Lys Phe Lys Asp Ile Phe Gly Asp Asp
165                               170                               175
Leu Tyr Leu Glu Leu Gln Ala Asn Asn Ile Pro Glu Gln Glu Val Ala
180                               185                               190
Asn Arg Asn Leu Ile Glu Ile Ala Lys Lys Tyr Asp Val Lys Leu Ile
195                               200                               205
Ala Thr Gln Asp Ala His Tyr Leu Asn Pro Glu Asp Arg Tyr Ala His
210                               215                               220
Thr Val Leu Met Ala Leu Gln Met Lys Lys Thr Ile His Glu Leu Ser
225                               230                               235                               240
Ser Gly Asn Phe Lys Cys Ser Asn Glu Asp Leu His Phe Ala Pro Pro
245                               250                               255
Glu Tyr Met Trp Lys Lys Phe Glu Gly Lys Phe Glu Gly Trp Glu Lys
260                               265                               270
Ala Leu Leu Asn Thr Leu Glu Val Met Glu Lys Thr Ala Asp Ser Phe
275                               280                               285
Glu Ile Phe Glu Asn Ser Thr Tyr Leu Leu Pro Lys Tyr Asp Val Pro
290                               295                               300
Pro Asp Lys Thr Leu Glu Glu Tyr Leu Arg Glu Leu Ala Tyr Lys Gly
305                               310                               315                               320
Leu Arg Gln Arg Ile Glu Arg Gly Gln Ala Lys Asp Thr Lys Glu Tyr
325                               330                               335
Trp Glu Arg Leu Glu Tyr Glu Leu Glu Val Ile Asn Lys Met Gly Phe
340                               345                               350
Ala Gly Tyr Phe Leu Ile Val Gln Asp Phe Ile Asn Trp Ala Lys Lys
355                               360                               365
Asn Asp Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Gly Gly Ser Leu
370                               375                               380
Val Ala Tyr Ala Ile Gly Ile Thr Asp Val Asp Pro Ile Lys His Gly
385                               390                               395                               400
Phe Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp
405                               410                               415
Ile Asp Val Asp Phe Cys Gln Asp Asn Arg Glu Lys Val Ile Glu Tyr
420                               425                               430
Val Arg Asn Lys Tyr Gly His Asp Asn Val Ala Gln Ile Ile Thr Tyr
435                               440                               445

```

Sequence Listing_R10901_Corrected.txt

```

Asn Val Met Lys Ala Lys Gln Thr Leu Arg Asp Val Ala Arg Ala Met
450                               455                               460

Gly Leu Pro Tyr Ser Thr Ala Asp Lys Leu Ala Lys Leu Ile Pro Gln
465                               470                               475                               480

Gly Asp Val Gln Gly Thr Trp Leu Ser Leu Glu Glu Met Tyr Lys Thr
                               485                               490                               495

Pro Val Glu Glu Leu Leu Gln Lys Tyr Gly Glu His Arg Thr Asp Ile
500                               505                               510

Glu Asp Asn Val Lys Lys Phe Arg Gln Ile Cys Glu Glu Ser Pro Glu
515                               520                               525

Ile Lys Gln Leu Val Glu Thr Ala Leu Lys Leu Glu Gly Leu Thr Arg
530                               535                               540

His Thr Ser Leu His Ala Ala Gly Val Val Ile Ala Pro Lys Pro Leu
545                               550                               555                               560

Ser Glu Leu Val Pro Leu Tyr Tyr Asp Lys Glu Gly Glu Val Ala Thr
565                               570                               575

Gln Tyr Asp Met Val Gln Leu Glu Glu Leu Gly Leu Leu Lys Met Asp
580                               585                               590

Phe Leu Gly Leu Lys Thr Leu Thr Glu Leu Lys Leu Met Lys Glu Leu
595                               600                               605

Ile Lys Glu Arg His Gly Val Asp Ile Asn Phe Leu Glu Leu Pro Leu
610                               615                               620

Asp Asp Pro Lys Val Tyr Gln Lys Leu Leu Gln Glu Gly Lys Thr Thr Gly
625                               630                               635                               640

Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu Leu Leu Lys Lys Leu
645                               650                               655

Lys Pro Asp Ser Phe Asp Asp Ile Val Ala Val Leu Ala Leu Tyr Arg
660                               665                               670

Pro Gly Pro Leu Lys Ser Gly Leu Val Asp Thr Tyr Ile Lys Arg Lys
675                               680                               685

His Gly Lys Glu Pro Val Glu Tyr Pro Phe Pro Glu Leu Glu Pro Val
690                               695                               700

Leu Lys Glu Thr Tyr Gly Val Ile Val Tyr Gln Glu Gln Val Met Lys
705                               710                               715                               720

Met Ser Gln Ile Leu Ser Gly Phe Thr Pro Gly Glu Ala Asp Thr Leu
725                               730                               735

Arg Lys Ala Ile Gly Lys Lys Lys Ala Asp Leu Met Ala Gln Met Lys
740                               745                               750

Asp Lys Phe Ile Gln Gly Ala Val Glu Arg Gly Tyr Pro Glu Glu Lys
755                               760                               765

```


Sequence_Listing_R10901_Corrected.txt

```

Ile Arg Lys Leu Trp Glu Asp Ile Glu Lys Phe Ala Ser Tyr Ser Phe
770                               775                               780

Asn Lys Ser His Ser Val Ala Tyr Gly Tyr Ile Ser Tyr Trp Thr Ala
785                               790                               795                               800

Tyr Val Lys Ala His Tyr Pro Ala Glu Phe Phe Ala Val Lys Leu Thr
805                               810                               815

Thr Glu Lys Asn Asp Asn Lys Phe Leu Asn Leu Ile Lys Asp Ala Lys
820                               825                               830

Leu Phe Gly Phe Glu Ile Leu Pro Pro Asp Ile Asn Lys Ser Asp Val
835                               840                               845

Gly Phe Thr Ile Glu Gly Glu Asn Arg Ile Arg Phe Gly Leu Ala Arg
850                               855                               860

Ile Lys Gly Val Gly Glu Glu Thr Ala Lys Ile Ile Val Glu Ala Arg
865                               870                               875                               880

Lys Lys Tyr Lys Gln Phe Lys Gly Leu Ala Asp Phe Ile Asn Lys Thr
885                               890                               895

Lys Asn Arg Lys Ile Asn Lys Lys Val Val Glu Ala Leu Val Lys Ala
900                               905                               910

Gly Ala Phe Asp Phe Thr Lys Lys Lys Arg Lys Glu Leu Leu Ala Lys
915                               920                               925

Val Ala Asn Ser Glu Lys Ala Leu Met Ala Thr Gln Asn Ser Leu Phe
930                               935                               940

Gly Ala Pro Lys Glu Glu Val Glu Glu Leu Asp Pro Leu Lys Leu Glu
945                               950                               955                               960

Lys Glu Val Leu Gly Phe Tyr Ile Ser Gly His Pro Leu Asp Asn Tyr
965                               970                               975

Glu Lys Leu Leu Lys Asn Arg Tyr Thr Pro Ile Glu Asp Leu Glu Glu
980                               985                               990

Trp Asp Lys Glu Ser Glu Ala Val Leu Thr Gly Val Ile Thr Glu Leu
995                               1000                               1005

Lys Val Lys Lys Thr Lys Asn Gly Asp Tyr Met Ala Val Phe Asn Leu
1010                               1015                               1020

Val Asp Lys Thr Gly Leu Ile Glu Cys Val Val Phe Pro Gly Val Tyr
1025                               1030                               1035                               1040

Glu Glu Ala Lys Glu Leu Ile Glu Glu Asp Arg Val Val Val Val Lys
1045                               1050                               1055

Gly Phe Leu Asp Glu Asp Leu Glu Thr Glu Asn Val Lys Phe Val Val
1060                               1065                               1070

Lys Glu Val Phe Ser Pro Glu Glu Phe Ala Lys Glu Met Arg Asn Thr

```

Sequence_Listing_R1090i_Corrected.txt
1075 1080 1085

Leu Tyr Ile Phe Leu Lys Arg Glu Gln Ala Leu Asn Gly Val Ala Glu
1090 1095 1100

Lys Leu Lys Gly Ile Ile Glu Asn Asn Arg Thr Glu Asp Gly Tyr Asn
1105 1110 1115 1120

Leu Val Leu Thr Val Asp Leu Gly Asp Tyr Phe Val Asp Leu Ala Leu
1125 1130 1135

Pro Gln Asp Met Lys Leu Lys Ala Asp Arg Lys Val Val Glu Glu Ile
1140 1145 1150

Glu Lys Leu Gly Val Lys Val Ile Ile
1155 1160

<210> 119
<211> 2408
<212> DNA
<213> Aquifex aeolicus

<400> 119
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caggaagctc ccgtaaggat actcaaaaaa gctataaaaa acgacagagt ggctcagcgc 120
tacctctttg ccggaccagag ggggggttggg aagacgacta ttgcaagaat tctcgcaaaa 180
cgttttgaaat gtataaaatcc ctccaaaggt gagccctgag gtgagtgcca aaactgcagg 240
gagatagaca ggggtgtgatt ccttgactta attgaaatgg atgcgcgctc aaacacgggt 300
atagacgacg taagggtcatt aaaagaagcg gtcaattaca aacctataaa aggaaggtac 360
aagggtttaca taatagacga agctcacatg ctacagaaag aagctttcaa cgctctctta 420
aaaacccctc aagagccccc tcccagaact gttttctgcc ttgtaccac ggagtagcac 480
aaaattcttc ccacgatact ctcaaggtgt cagaggataa tcttctcaaa ggtaagaaag 540
gaaaagtaa tagagtattc aaaaagata tgtgaaagg aagggtatga gtgcgaagag 600
ggagcccttg aggttctcgt tcatgcctct gaagggtgca tgagggtgac accctctctc 660
ctggaccagg cgagcgttta cggggaagcg agggtaacaa aagaagtatg ggagaacttc 720
ctcggaattc tcagtcagga aagcgttagg agttttctga aattgcttct gaactcagaa 780
gtggaccgaag ctataaagtt cctcagagaa ctctcagaaa agggctacaa cctgaccaag 840
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cccgaaagcg tggttcagaa ctggcaggat tacgaagact tcaaagacta cctctggaa 960
gcctctctct acgttgagaa cctgataaac aggggtaaa ttgaagcgag aacgagagaa 1020
cccttaagag cctttgaact cgcggtataa aagagcctta tagtcaaaaga cataattccc 1080
gtatccagc tcggaagtgt ggttaagaaa accaaaaagg aagaaagaaa aggttgagta 1140
aaagaagcgc aaaaagttaa agaaagaaa ccaaaaggag aggaagagga caggttccag 1200
aaagttttaa acgctgtgga cggcaaaatc cttaaaagaa tacttgaagg ggcaaaaaag 1260
gaagaagaag acggaaaaaa cgtctctaaa atagaagcct ctattctgag aacctgtaaa 1320
aaggaatttg actcactaaa ggagactttt ctttttttag agtttgaacc cgtggaggat 1380
aaaaaaaaa ctacagaagtc cagcgggacg aggtctgttt aaaggttaa gactcttca 1440
atgcataaat actcaaaagt cgaagttaaa gctaaaggtc taaaggtgag aatgcccggt 1500
gaagagatag ggctgtttaa cgcactaata gacggtctgc ccaggtacgc actcacagg 1560
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ttgatggaag ctatggaggg tatgaaaaaa cactataaagg atttgaagaa cctcgagag 1680
acggtggaag atttaacttt ttaaaagtat ggtgtatctg agcaaaaggt taagctaaaa 1740
acaaacctga aaccgcagcg ggccacgacg aaagccataa aaaaactcct tgaaaaacct 1800
aggaagagcg taaaagaaaca aacactcttc ggaatcacgg gaagcggaag gaactttact 1860
ctgcgcaaac taatagcgaa gtacaaacaa ccaactcttg tgttagitca caacaaaatt 1920
cttcgcgcaac agctatacac ggaagtttaa gaactattcc ctgaaaacgc tgtagagtac 1980
tttgtctctt actacgacta ttaccaacct gaagcctaca tttccgaaaa agatttatac 2040
atagaaaagg acgcgagtat aaacgaaagc tgaagacttt cagacactcc gccacgatat 2100

Sequence_Listing_R10901_Corrected.txt

```

ccgttctaga aaggaggagac gttatagtag ttgcttcagt ttccttgcata tacggactcg 2160
ggaaacctga gcactacgaa aacctgagga taaaactcca aagggaata agactgaact 2220
tgaqtaagct cctgaggaaa ctgcttgagc taggatatac gagaatgac tttgccataa 2280
agagggctac cttctcggtt aggggagacg tgggttgagat agtcccttct cacacggaag 2340
attacctcgt gagggtagag ttctgggacg acgaagttag aagaatagtc ctcacggagc 2400
ctctgaac 2408

```

<210> 120

<211> 473

<212> PRT

<213> Aquifex aeolicus

<400> 120

```

Met Asn Tyr Val Pro Phe Ala Arg Lys Tyr Arg Pro Lys Phe Phe Arg
 1             5             10             15

```

```

Glu Val Ile Gly Gln Glu Ala Pro Val Arg Ile Leu Lys Asn Ala Ile
      20             25             30

```

```

Lys Asn Asp Arg Val Ala His Ala Tyr Leu Phe Ala Gly Pro Arg Gly
      35             40             45

```

```

Val Gly Lys Thr Thr Ile Ala Arg Ile Leu Ala Lys Ala Leu Asn Cys
      50             55             60

```

```

Lys Asn Pro Ser Lys Gly Glu Pro Cys Gly Glu Cys Glu Asn Cys Arg
      65             70             75             80

```

```

Glu Ile Asp Arg Gly Val Phe Pro Asp Leu Ile Glu Met Asp Ala Ala
      85             90             95

```

```

Ser Asn Arg Gly Ile Asp Asp Val Arg Ala Leu Lys Glu Ala Val Asn
     100             105             110

```

```

Tyr Lys Pro Ile Lys Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Ala
     115             120             125

```

```

His Met Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
     130             135             140

```

```

Glu Pro Pro Pro Arg Thr Val Phe Val Leu Cys Thr Thr Glu Tyr Asp
     145             150             155             160

```

```

Lys Ile Leu Pro Thr Ile Leu Ser Arg Cys Gln Arg Ile Ile Phe Ser
     165             170             175

```

```

Lys Val Arg Lys Glu Lys Val Ile Glu Tyr Leu Lys Lys Ile Cys Glu
     180             185             190

```

```

Lys Glu Gly Ile Glu Cys Glu Glu Gly Ala Leu Glu Val Leu Ala His
     195             200             205

```

```

Ala Ser Glu Gly Cys Met Arg Asp Ala Ala Ser Leu Leu Asp Gln Ala
     210             215             220

```

```

Ser Val Tyr Gly Glu Gly Arg Val Thr Lys Glu Val Val Glu Asn Phe
     225             230             235             240

```

Sequence Listing_R10901_Corrected.txt

Leu Gly Ile Leu Ser Gln Glu Ser Val Arg Ser Phe Leu Lys Leu Leu
 245 250 255
 Leu Asn Ser Glu Val Asp Glu Ala Ile Lys Phe Leu Arg Glu Leu Ser
 260 265 270
 Glu Lys Gly Tyr Asn Leu Thr Lys Phe Trp Glu Met Leu Glu Glu Glu
 275 280 285
 Val Arg Asn Ala Ile Leu Val Lys Ser Leu Lys Asn Pro Glu Ser Val
 290 295 300
 Val Gln Asn Trp Gln Asp Tyr Glu Asp Phe Lys Asp Tyr Pro Leu Glu
 305 310 315 320
 Ala Leu Leu Tyr Val Glu Asn Leu Ile Asn Arg Gly Lys Val Glu Ala
 325 330 335
 Arg Thr Arg Glu Pro Leu Arg Ala Phe Glu Leu Ala Val Ile Lys Ser
 340 345 350
 Leu Ile Val Lys Asp Ile Ile Pro Val Ser Gln Leu Gly Ser Val Val
 355 360 365
 Lys Glu Thr Lys Lys Glu Glu Lys Lys Val Glu Val Lys Glu Glu Pro
 370 375 380
 Lys Val Lys Glu Glu Lys Pro Lys Glu Gln Glu Glu Asp Arg Phe Gln
 385 390 395 400
 Lys Val Leu Asn Ala Val Asp Gly Lys Ile Leu Lys Arg Ile Leu Glu
 405 410 415
 Gly Ala Lys Arg Glu Glu Arg Asp Gly Lys Ile Val Leu Lys Ile Glu
 420 425 430
 Ala Ser Tyr Leu Arg Thr Met Lys Lys Glu Phe Asp Ser Leu Lys Glu
 435 440 445
 Thr Phe Pro Phe Leu Glu Phe Glu Pro Val Glu Asp Lys Lys Lys Pro
 450 455 460
 Gln Lys Ser Ser Gly Thr Arg Leu Phe
 465 470

<210> 121

<211> 1090

<212> DNA

<213> Aquifex aeolicus

<400> 121

atgcgcgttta aggtggacag ggaggagcctt gaagaggttc ttaaaaaaac aagagaaaac 60
 acggaaaaaa aagccgcact cccgatactc gcgaacttct tactctccgc aaaagaggaa 120
 aacttaatcg taagggcacac gaacttggaa aactaccttg tagtctccgt aaagggggag 180
 gttgaagagg aaggagaggt ttgcgtccac tctcaaaaaac tctacgatat agtcaagaac 240
 ttaattccg cttacgttta ccttcatacg gaaggtgaaa aactcgtcat aacgggagga 300
 aagagtacgt acaaaacttc gacagctccc gcggaggact ttcccgaatt tccagaaatc 360
 gtagaaggag gagaacact ttccggaaac ctctcgttta acggaataga aaaggtagag 420

Sequence_Listing_R10901_Corrected.txt

```

tacgccatag cgaaggaaga agcgaacata gcccttcagg gaatgtatct gagaggatcac 480
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taaacattga aaagagtgaa gacgagtcct ttgcttactt ctcactcccg gagtggaac 600
tcggcggttag ctcctggaag gagaattccc ggaactacatg agtgtcatcc ctgaggagtt 660
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agcgaaaagg tgtggttcaa gttcacaaac ccgcacaacg ccactttatt ggagcgtgaa 960
gattacgaaa aggaacctta caagtgcata ataatgcga tgaggggtga gccatgaaaa 1020
aagctttaat cttttatttg agcttgagcc tttaatttcc tgcgttttagc gaagcctaac 1080
ccaagtcttc

```

<210> 122

<211> 363

<212> PRT

<213> Aquifex aeolicus

<400> 122

```

Met Arg Val Lys Val Asp Arg Glu Glu Leu Glu Val Leu Lys Lys
 1             5             10            15
Ala Arg Glu Ser Thr Glu Lys Lys Ala Ala Leu Pro Ile Leu Ala Asn
 20             25
Phe Leu Leu Ser Ala Lys Glu Glu Asn Leu Ile Val Arg Ala Thr Asp
 35             40            45
Leu Glu Asn Tyr Leu Val Val Ser Val Lys Gly Glu Val Glu Glu Glu
 50             55            60
Gly Glu Val Cys Val His Ser Gln Lys Leu Tyr Asp Ile Val Lys Asn
 65             70            75            80
Leu Asn Ser Ala Tyr Val Tyr Leu His Thr Glu Gly Glu Lys Leu Val
 85             90            95
Ile Thr Gly Gly Lys Ser Thr Tyr Lys Leu Pro Thr Ala Pro Ala Glu
100            105            110
Asp Phe Pro Glu Phe Pro Glu Ile Val Glu Gly Gly Glu Thr Leu Ser
115            120            125
Gly Asn Leu Leu Val Asn Gly Ile Glu Lys Val Glu Tyr Ala Ile Ala
130            135            140
Lys Glu Glu Ala Asn Ile Ala Leu Gln Gly Met Tyr Leu Arg Gly Tyr
145            150            155            160
Glu Asp Arg Ile His Phe Val Gly Ser Asp Gly His Arg Leu Ala Leu
165            170            175
Tyr Glu Pro Leu Gly Glu Phe Ser Lys Glu Leu Leu Ile Pro Arg Lys
180            185            190
Ser Leu Lys Val Leu Lys Lys Leu Ile Thr Gly Ile Glu Asp Val Asn
195            200            205

```

Sequence Listing_R10901_Corrected.txt

Ile Glu Lys Ser Glu Asp Glu Ser Phe Ala Tyr Phe Ser Thr Pro Glu
210 215 220

Trp Lys Leu Ala Val Arg Leu Leu Glu Gly Glu Phe Pro Asp Tyr Met
225 230 235 240

Ser Val Ile Pro Glu Glu Phe Ser Ala Glu Val Leu Phe Glu Thr Glu
245 250 255

Glu Val Leu Lys Val Leu Lys Arg Leu Lys Ala Leu Ser Glu Gly Lys
260 265 270

Val Phe Pro Val Lys Ile Thr Leu Ser Glu Asn Leu Ala Ile Phe Glu
275 280 285

Phe Ala Asp Pro Glu Phe Gly Glu Ala Arg Glu Glu Ile Glu Val Glu
290 295 300

Tyr Thr Gly Glu Pro Phe Glu Ile Gly Phe Asn Gly Lys Tyr Leu Met
305 310 315 320

Glu Ala Leu Asp Ala Tyr Asp Ser Glu Arg Val Trp Phe Lys Phe Thr
325 330 335

Thr Pro Asp Thr Ala Thr Leu Leu Glu Ala Glu Asp Tyr Glu Lys Glu
340 345 350

Pro Tyr Lys Cys Ile Ile Met Pro Met Arg Val
355 360

<210> 123

<211> 1093

<212> DNA

<213> Aquifex aeolicus

<400> 123

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gaaaagtacg gggagaatta cacggttcctg tggggggatg agataaagcga ggaggaattc 180
tacaactgcc ttcccgagac cagtatattc ggcggttcaa aggaaaaagc ggtggtcatt 240
tacaactctg gggatttctt gaagaagctc ggaagggaaga aaaaggaaaa agaaaggctt 300
taaaaagtcc tcagaaacctg aaagagtaac tacgtattta tagtgtacga tgcgaaacct 360
cagaaacagg aacttttctc ggaacctctg aaatccgtag cgtctttcgg cggtatagt 420
gtagcaaaaa ggcctagcaa ggagaggata aaacagctcg tcttaagaa gttcaaaaga 480
aaagggataa acgtagaaaa cgtatgccctt gaataccttc tccagctcac gggttaacac 540
ttgatggagc tcaaaactga ggttgaaaaa ctgatagatt acgcaagtga aaagaaaaatt 600
ttaacactcg attgagtaaa gagagtagcc ttctcagctc cagaaaaagc aaacgtattt 660
gagttcgttg atttactcct cttaaaagat tacgaaaagg ctcttaaaagt tttggactcc 720
ctcaattctc tgggaataca cccctccag attatgaaaa tctgtctctc ctatgctcta 780
aaactttaca cctcaagag gcttgaagag aaggagagg aactgaataa ggcgatggaa 840
agcgtgggaa taaagaacaa ctttctcaag atgaagtcca aatcttactt aaaggcaaac 900
tctaaagagg acctgaagaa cctaactctc tccctccaga ggatagacgc ttttctaaa 960
ctttactttc aggacacagt gtagttgctg gggattttctt gacctcaaga ctggagagg 1020
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ttttcccggt tct                                     1093

```

<210> 124

Sequence_Listing_R10901_Corrected.txt

<211> 350

<212> PRT

<213> Aquifex aeolicus

<400> 124

```

Val Glu Thr Thr Ile Phe Gln Phe Gln Lys Thr Phe Phe Thr Lys Pro
 1           5           10           15

Pro Lys Glu Arg Val Phe Val Leu His Gly Glu Glu Gln Tyr Leu Ile
      20           25           30

Arg Thr Phe Leu Ser Lys Leu Lys Glu Lys Tyr Gly Glu Asn Tyr Thr
      35           40           45

Val Leu Trp Gly Asp Glu Ile Ser Glu Glu Glu Phe Tyr Thr Ala Leu
      50           55           60

Ser Glu Thr Ser Ile Phe Gly Gly Ser Lys Glu Lys Ala Val Val Ile
      65           70           75           80

Tyr Asn Phe Gly Asp Phe Leu Lys Lys Leu Gly Arg Lys Lys Lys Glu
      85           90           95

Lys Glu Arg Leu Ile Lys Val Leu Arg Asn Val Lys Ser Asn Tyr Val
      100          105          110

Phe Ile Val Tyr Asp Ala Lys Leu Gln Lys Gln Glu Leu Ser Ser Glu
      115          120          125

Pro Leu Lys Ser Val Ala Ser Phe Gly Gly Ile Val Val Ala Asn Arg
      130          135          140

Leu Ser Lys Glu Arg Ile Lys Gln Leu Val Leu Lys Lys Phe Lys Glu
      145          150          155          160

Lys Gly Ile Asn Val Glu Asn Asp Ala Leu Glu Tyr Leu Leu Gln Leu
      165          170          175

Thr Gly Tyr Asn Leu Met Glu Leu Lys Leu Glu Val Glu Lys Leu Ile
      180          185          190

Asp Tyr Ala Ser Glu Lys Lys Ile Leu Thr Leu Asp Glu Val Lys Arg
      195          200          205

Val Ala Phe Ser Val Ser Glu Asn Val Asn Val Phe Glu Phe Val Asp
      210          215          220

Leu Leu Leu Leu Lys Asp Tyr Glu Lys Ala Leu Lys Val Leu Asp Ser
      225          230          235          240

Leu Ile Ser Phe Gly Ile His Pro Leu Gln Ile Met Lys Ile Leu Ser
      245          250          255

Ser Tyr Ala Leu Lys Leu Tyr Thr Leu Lys Arg Leu Glu Glu Lys Gly
      260          265          270

Glu Asp Leu Asn Lys Ala Met Glu Ser Val Gly Ile Lys Asn Asn Phe
      275          280          285

```

Sequence_Listing_R10901_Corrected.txt

Leu Lys Met Lys Phe Lys Ser Tyr Leu Lys Ala Asn Ser Lys Glu Asp
290 295 300

Leu Lys Asn Leu Ile Leu Ser Leu Gln Arg Ile Asp Ala Phe Ser Lys
305 310 315 320

Leu Tyr Phe Gln Asp Thr Val Gln Leu Leu Arg Asp Phe Leu Thr Ser
325 330 335

Arg Leu Glu Arg Glu Val Val Lys Asn Thr Ser His Gly Gly
340 345 350

<210> 125

<211> 1051

<212> DNA

<213> Aquifex aeolicus

<400> 125

atggaaaaag tttttttgga aaaactccag aaaaccttgc acatacccgaggaggactcctt 60
ttttacggca aagaaggaag cggaaagacg aaaacagctt ttgaatttgc aaaaggtatt 120
ttatgtaagg aaaacgtacc tggggatgcg gaagtgtgcc ctccgcaaaa caccgtaaacg 180
agctggagga agcctctctt aaaggagaaa tagaagactt taagtttat aagcaagga 240
cggtaaaaag cacttcgttt accttatggg cgaacatccc gactttgtgg taataatccc 300
gagcggacat tacataaaga tagaacagat aagggaagtt aagaactttg cctatgtgaa 360
gcccgcaact agcaggagaa aagtaattat aatagacgac gccacgcgga tgacctctca 420
ggcgcaaac gctcttttaa aggtattgga agagccacct gggacacca cctttattct 480
gaccacgaac aggcgttctg caatcctgcc gactatcctc tcacagaact ttcaagtggga 540
gttcaagggc ttttcagtaa aagaggttat ggaaatagcg aaagttagagc aggaaatagc 600
gaaactctct ggaggcagtc taaaaagggc tatcttacta aaggaaaaa aagatatcct 660
aaacaaagta aaggaaattct tggaaaaaga gccgttataa gtttacaagc ttgcaagtga 720
attcgaaaag tgggaacctg aaaagcaaaa actcttctct gaattatgg aagaatttgt 780
attcaaaaaa ttgaccgaag agaaaaaaga caattacacc taccttcttg atacgatcag 840
actctttaa gacggactcg caagggtgt aaacgaacct ctgtggctgt ttacgttagc 900
cgttcaggcg gattaataaa ccgttatgta ttccgtaaca tttaaacctt aatctaaatt 960
atgagagcct ttgaaggagg tctggtatgg aaaatttgaa gattagatat atagatacga 1020
ggaagatagg aaccgtgagc ggtgtaaaag t 1051

<210> 126

<211> 305

<212> PRT

<213> Aquifex aeolicus

<400> 126

Met Glu Lys Val Phe Leu Glu Lys Leu Gln Lys Thr Leu His Ile Pro
1 5 10 15

Gly Gly Leu Leu Phe Tyr Gly Lys Glu Gly Ser Gly Lys Thr Lys Thr
20 25 30

Ala Phe Glu Phe Ala Lys Gly Ile Leu Cys Lys Glu Asn Val Pro Trp
35 40 45

Gly Cys Gly Ser Cys Pro Ser Cys Lys His Val Asn Glu Leu Glu Glu
50 55 60

Ala Phe Phe Lys Gly Glu Ile Glu Asp Phe Lys Val Tyr Lys Asp Lys
65 70 75 80

Sequence_Listing_R10901_Corrected.txt

```

Asp Gly Lys Lys His Phe Val Tyr Leu Met Gly Glu His Pro Asp Phe
      85                      90                      95

Val Val Ile Ile Pro Ser Gly His Tyr Ile Lys Ile Glu Gln Ile Arg
      100                      105                      110

Glu Val Lys Asn Phe Ala Tyr Val Lys Pro Ala Leu Ser Arg Arg Lys
      115                      120                      125

Val Ile Ile Ile Asp Asp Ala His Ala Met Thr Ser Gln Ala Ala Asn
      130                      135                      140

Ala Leu Leu Lys Val Leu Glu Glu Pro Pro Ala Asp Thr Thr Phe Ile
      145                      150                      155                      160

Leu Thr Thr Asn Arg Arg Ser Ala Ile Leu Pro Thr Ile Leu Ser Arg
      165                      170                      175

Thr Phe Gln Val Glu Phe Lys Gly Phe Ser Val Lys Glu Val Met Glu
      180                      185                      190

Ile Ala Lys Val Asp Glu Glu Ile Ala Lys Leu Ser Gly Gly Ser Leu
      195                      200                      205

Lys Arg Ala Ile Leu Leu Lys Glu Asn Lys Asp Ile Leu Asn Lys Val
      210                      215                      220

Lys Glu Phe Leu Glu Asn Glu Pro Leu Lys Val Tyr Lys Leu Ala Ser
      225                      230                      235                      240

Glu Phe Glu Lys Trp Glu Pro Glu Lys Gln Lys Leu Phe Leu Glu Ile
      245                      250                      255

Met Glu Glu Leu Val Ser Gln Lys Leu Thr Glu Glu Lys Lys Asp Asn
      260                      265                      270

Tyr Thr Tyr Leu Leu Asp Thr Ile Arg Leu Phe Lys Asp Gly Leu Ala
      275                      280                      285

Arg Gly Val Asn Glu Pro Leu Trp Leu Phe Thr Leu Ala Val Gln Ala
      290                      295                      300

```

Asp
305

<210> 127
 <211> 630
 <212> DNA
 <213> Aquifex aeolicus

```

<400> 127
atgaacttcc tgaaaaagtt ccttttactg agaaaagctc aaaagtctcc ttacttcgaa 60
gagttctacg aagaaatcga tttagaacceg aaggtgaaag atgcaagggt ttagtatttt 120
gactgcgaag ccacagaact cgacgtaaag aaggcaaaac tcctttcaat aggtgcggtt 180
gagggttaaa accctggaaat agacctctct aaatctttt acgagatact caaaagtgc 240
gagataaagg cgcgggagat acatggaata accagggaag acgttgaaaa gtacggaaag 300
gaaccaaaag aagtaataata cgactttctg aagtaacataa agggaagcgt tctcgttgcc 360

```

Sequence_Listing_R10901_Corrected.txt

```
tactacgtga agtttgacgt ctcaactcgtt gagaagtact ccataaagta cttccagtat 420
ccaatcatca actacaagtt agacctgttt agtttcgtga agagagagta ccagagtggc 480
aggagctttg acgaccttat gaaggaactc ggtgtagaaa taagggccaag gcacaacgcc 540
cttgaagatg cctacataac cgctcttctt ttccataaagt acgtttaccg gaacagggag 600
tacagactaa aggatctccc gattttcctt                                     630
```

<210> 128

<211> 210

<212> PRT

<213> Aquifex aeolicus

<400> 128

```
Met Asn Phe Leu Lys Lys Phe Leu Leu Arg Lys Ala Gln Lys Ser
 1          5          10          15

Pro Tyr Phe Glu Glu Phe Tyr Glu Glu Ile Asp Leu Asn Gln Lys Val
      20          25          30

Lys Asp Ala Arg Phe Val Val Phe Asp Cys Glu Ala Thr Glu Leu Asp
      35          40          45

Val Lys Lys Ala Lys Leu Leu Ser Ile Gly Ala Val Glu Val Lys Asn
      50          55          60

Leu Glu Ile Asp Leu Ser Lys Ser Phe Tyr Glu Ile Leu Lys Ser Asp
      65          70          75          80

Glu Ile Lys Ala Ala Glu Ile His Gly Ile Thr Arg Glu Asp Val Glu
      85          90          95

Lys Tyr Gly Lys Glu Pro Lys Glu Val Ile Tyr Asp Phe Leu Lys Tyr
      100          105          110

Ile Lys Gly Ser Val Leu Val Gly Tyr Tyr Val Lys Phe Asp Val Ser
      115          120          125

Leu Val Glu Lys Tyr Ser Ile Lys Tyr Phe Gln Tyr Pro Ile Ile Asn
      130          135          140

Tyr Lys Leu Asp Leu Phe Ser Phe Val Lys Arg Glu Tyr Gln Ser Gly
      145          150          155          160

Arg Ser Leu Asp Asp Leu Met Lys Glu Leu Gly Val Glu Ile Arg Ala
      165          170          175

Arg His Asn Ala Leu Glu Asp Ala Tyr Ile Thr Ala Leu Leu Phe Leu
      180          185          190

Lys Tyr Val Tyr Pro Asn Arg Glu Tyr Arg Leu Lys Asp Leu Pro Ile
      195          200          205

Phe Leu
      210
```

<210> 129

<211> 526

<212> DNA

Sequence_Listing_R10901_Corrected.txt

<213> Aquifex aeolicus

<400> 129

```

atgctcaata aggtttttat aataggaaga cttaagggtg accccgttat aacttatcta 60
ccgagcggaa cccccgtagt agagtttact ctggcttaca acagaaggta taaaaccag 120
aacggtgaat ttcaggagga aagtcacttc ttgacgtaa aggcgtacgg aaaaatggct 180
gaagactggg ctacacgctt ctgaaagga tacctcgtac tctgtagagg aagactctcc 240
caggaaaagt gggagaaaga aggaagaag ttctcaaag tcaggataat agcggaaaac 300
gtaagattaa taaacaggcc gaaagggtgt gaacttcaag cagaagaaga ggagggaagt 360
cctccatttg aggaggaagt tgaaaaaactc ggtaaagagg aagagaagcc ttttaccgat 420
gaagaggacg aaataaccttt ttaattttga ggagggttaa gtatggtagt gagagctcct 480
aagaagaag ttgtatgta ctgtgaacaa aagagagagc cagatt 526

```

<210> 130

<211> 147

<212> PRT

<213> Aquifex aeolicus

<400> 130

```

Met Leu Asn Lys Val Phe Ile Ile Gly Arg Leu Thr Gly Asp Pro Val
  1             5             10             15

Ile Thr Tyr Leu Pro Ser Gly Thr Pro Val Val Glu Phe Thr Leu Ala
                20             25             30

Tyr Asn Arg Arg Tyr Lys Asn Gln Asn Gly Glu Phe Gln Glu Glu Ser
        35             40             45

His Phe Phe Asp Val Lys Ala Tyr Gly Lys Met Ala Glu Asp Trp Ala
        50             55             60

Thr Arg Phe Ser Lys Gly Tyr Leu Val Leu Val Glu Gly Arg Leu Ser
        65             70             75             80

Gln Glu Lys Trp Glu Lys Glu Gly Lys Lys Phe Ser Lys Val Arg Ile
        85             90             95

Ile Ala Glu Asn Val Arg Leu Ile Asn Arg Pro Lys Gly Ala Glu Leu
        100            105            110

Gln Ala Glu Glu Glu Glu Glu Val Pro Pro Ile Glu Glu Glu Ile Glu
        115            120            125

Lys Leu Gly Lys Glu Glu Glu Lys Pro Phe Thr Asp Glu Glu Asp Glu
        130            135            140

Ile Pro Phe
145

```

<210> 131

<211> 1472

<212> DNA

<213> Aquifex aeolicus

<400> 131

```

atgcaatttg tggataaact tccctgtgac gaatccgccg agaggcggtg tcttggcagt 60
atgcttgaag accccgaaaa catacctctg gtacttgaat accttaaga agaagacttc 120

```

Sequence_Listing_R10901_Corrected.txt

```

tgcataagacg agcacaaagct acttttcagg gttcttcaaa accctctggc cgagtagggc 180
aataagctcg atttcgtatt aataaaggat cacottgaaa agaaaaaactt actccagaaa 240
ataacctatag actggctcga agaactctac gaggaggcgg tatccctcga cagcgttgag 300
gaagctcgcga aaatagtaaa acaacgttcc gcacagaggg cgataattca actcgggtata 360
gaactcattc acaaaaggaaa ggaatacaaa gactttcaca cattaatcga ggaagcccaag 420
agcaggatatt ttcccatagc ggaaagtgcct acatctacgc agttttacca tggaaagac 480
gttcgggaag aagttataga actcatlta aaattcaaaa gctctgacag gctagtccag 540
ggactccaaa cgggtttcac ggaactcgat ctaaagacga cgggattcca cctcggagac 600
ttaataatac tcgcgcgaag acccgggtat gggaaaaacc cctttatgct ctccataatc 660
tacaactctc caaaagacga gggaaaaccc tcagctgtat ttcccttgga aatgagcaag 720
gaaacgctcg ttatgagact cctctctatg atgtcggagg tcccactttt caagataaag 780
ctcggaaata tatcgaatga agattttaa aagcttgaag caacgcgaat agaactcgca 840
aagtaacga aatacctcga cgacacaccc gctctcacta caacggattt aaggataaag 900
gcaagaaagc tcagaaagga aaaggaagtt gagttcgtgg cggcggaacta cttgcaactt 960
ctgagacccg cagtcocgaaa gacttcaaga caggaggaag tggcagaggt tccaagaaaac 1020
ttaaaagccc ttgcaaaagg acttcacatt cccgttatgg caactgcgca gctctccctg 1080
gaggttgaaa agaggagtg taaaaagccc cagcttgagg acctcagaga atccggagac 1140
atagaacagg acgcagacot aatccttttc ctccacagac ccgagtacta caagaataag 1200
ccaaatcccg aagagcaggg tatagcggaa gtgataatag ccaagcaaa gcnaggaccc 1260
acggacattg tgaagctcgc atttattaag gactacacta agtttgcaaa cctagaagcc 1320
ctctctgaac aaactctcga agaagaggaa ctttcgaaa ttattgaaac acaggaggat 1380
gaaggattcg aagatattga cttctgaaaa ttaaggtttt ataattttat cttggctatc 1440
cgggtagct caatcgcgag agcgggtggc tg 1472

```

<210> 132

<211> 438

<212> PRT

<213> Aquifex aeolicus

<400> 132

```

Met Gln Phe Val Asp Lys Leu Pro Cys Asp Glu Ser Ala Glu Arg Ala
 1          5          10          15
Val Leu Gly Ser Met Leu Glu Asp Pro Glu Asn Ile Pro Leu Val Leu
 20          25          30
Glu Tyr Leu Lys Glu Glu Asp Phe Cys Ile Asp Glu His Lys Leu Leu
 35          40          45
Phe Arg Val Leu Thr Asn Leu Trp Ser Glu Tyr Gly Asn Lys Leu Asp
 50          55          60
Phe Val Leu Ile Lys Asp His Leu Glu Lys Lys Asn Leu Leu Gln Lys
 65          70          75          80
Ile Pro Ile Asp Trp Leu Glu Glu Leu Tyr Glu Glu Ala Val Ser Pro
 85          90          95
Asp Thr Leu Glu Glu Val Cys Lys Ile Val Lys Gln Arg Ser Ala Gln
100          105          110
Arg Ala Ile Ile Gln Leu Gly Ile Thr Ser Thr Gln Phe Tyr His Val
115          120          125
Lys Asp Val Ala Glu Glu Val Ile Glu Leu Ile Tyr Lys Phe Lys Ser
130          135          140
Ser Asp Arg Leu Val Thr Gly Leu Pro Ser Gly Phe Thr Glu Leu Asp

```

Sequence_Listing_R10901_Corrected.txt

```

145          150          155          160
Leu Lys Thr Thr Gly Phe His Pro Gly Asp Leu Ile Ile Leu Ala Ala
    165          170          175
Arg Pro Gly Met Gly Lys Thr Ala Phe Met Leu Ser Ile Ile Tyr Asn
    180          185          190
Leu Ala Lys Asp Glu Gly Lys Pro Ser Ala Val Phe Ser Leu Glu Met
    195          200          205
Ser Lys Glu Gln Leu Val Met Arg Leu Leu Ser Met Met Ser Glu Val
    210          215          220
Pro Leu Phe Lys Ile Arg Ser Gly Ser Ile Ser Asn Glu Asp Leu Lys
    225          230          235
Lys Leu Glu Ala Ser Ala Ile Glu Leu Ala Lys Tyr Asp Ile Tyr Leu
    245          250          255
Asp Asp Thr Pro Ala Leu Thr Thr Thr Asp Leu Arg Ile Arg Ala Arg
    260          265          270
Lys Leu Arg Lys Glu Lys Glu Val Glu Phe Val Ala Val Asp Tyr Leu
    275          280          285
Gln Leu Leu Arg Pro Pro Val Arg Lys Ser Ser Arg Gln Glu Glu Val
    290          295          300
Ala Glu Val Ser Arg Asn Leu Lys Ala Leu Ala Lys Glu Leu His Ile
    305          310          315
Pro Val Met Ala Leu Ala Gln Leu Ser Arg Glu Val Glu Lys Arg Ser
    325          330          335
Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Gln Ile Glu
    340          345          350
Gln Asp Ala Asp Leu Ile Leu Phe Leu His Arg Pro Glu Tyr Tyr Lys
    355          360          365
Lys Lys Pro Asn Pro Glu Glu Gln Gly Ile Ala Glu Val Ile Ile Ala
    370          375          380
Lys Gln Arg Gln Gly Pro Thr Asp Ile Val Lys Leu Ala Phe Ile Lys
    385          390          395
Glu Tyr Thr Lys Phe Ala Asn Leu Glu Ala Leu Pro Glu Gln Pro Pro
    405          410          415
Glu Glu Glu Glu Leu Ser Glu Ile Ile Glu Thr Gln Glu Asp Glu Gly
    420          425          430
Phe Glu Asp Ile Asp Phe
    435

```

<210> 133

<211> 1526

Sequence_Listing_R10901_Corrected.txt

<212> DNA

<213> Aquifex aeolicus

<400> 133

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atgtctctcgg acatagacga acttagacgg gaaatagata tagtagacgt cacttcogaa 60
tactttaaact tagsgaaggt aggttccaat tacagaacga actgtccctt tcacctgac 120
gatacacccct ccttttaacgt gtctccaaagt aaacaaatat tcaagtgttt cggttgcggg 180
gtaggggggag acgcgataaa gtctcgtttcc ctttacgagg acatctccta ttttgaagcc 240
gcctctgaac tgcgaaaaacg ctacggaaaag aaattagacc ttgaaaagat atcaaaagac 300
gaaaagggtat acgtggctct tgacaggggt ttgtatttct acaggggaaag ccttctcaaa 360
aacagagagc caagtgaagta cgtaaaagagt aggggaatag accctaaagt agcggaggaag 420
tttgatcttg ggtacgcacc ttccagtgaa gcaactcgtaa aagtccttaa agagaacgat 480
cttttagagg cttaccttga aactaaaaac ctcttttctc ctacgaaggg tgtttacagg 540
gatctctttc ttccggcgtgt cgtgatcccgc ataaaggatc cgagggggaag agttataggt 600
ttcggtggaag ggaggatagt agaggacaaa tctcccaagt acataaactc tccagacagc 660
agggtattta aaaaggggga gaacttattc ggtctttacg aggcacagga gtatataaag 720
gaagaaggat ttgcgatact tgtggaaggg tactttgacc ttttgagact tttttccgag 780
ggaataaagg acgttgttgc acccctcggg acagccctga ccccaaatca ggcaaacctc 840
ctttccaaat tcacaaaaaa ggtctacalc ctttacgagc gagatgatgc gggaagaaag 900
gcatatgaaa gtgccattcc cctactcctc agtgacaggag tggaaagtta tcccgtttac 960
ctccccgaag gatacgtatcc cgcagagttt ataaaggaaat tcgggaaaga ggaattaaaga 1020
agactgataa acagctcagg ggagctcttt gaaacgctca taaaaaccgc aagggaataac 1080
ttagaggaga aaacgcgtga gttcaggtat tatctgggct ttatttcgca tggagtaagg 1140
cgctttgtct tggcttcgga gtttcacacc aagtacaaag ttctatgga aattttatta 1200
atgaaatttg aaaaaaatlc tcaagaaaaa gaaattaaac tctcctttaa gaaaaaaatc 1260
ttcctgaaag gactgataga attaaaacca aaaatagacc ttgaagtcct gaacttaagt 1320
cctgagttta aggaactcgc agttaacgcc ttaaacggag aggagcattt acttccaaaa 1380
gaagtctcag agtaccaggt ggataacttg gagaactttt ttaacaacat ccttaggat 1440
ttacaaaaat ctgggaaaaa gaggaagaaa agagggttga aaatgtaaa tacttaatta 1500
actttaataa atttttagag ttagga 1526

```

<210> 134

<211> 498

<212> PRT

<213> Aquifex aeolicus

<400> 134

```

Met Ser Ser Asp Ile Asp Glu Leu Arg Arg Glu Ile Asp Ile Val Asp
 1             5             10            15
Val Ile Ser Glu Tyr Leu Asn Leu Glu Lys Val Gly Ser Asn Tyr Arg
          20             25             30
Thr Asn Cys Pro Phe His Pro Asp Asp Thr Pro Ser Phe Tyr Val Ser
          35             40             45
Pro Ser Lys Gln Ile Phe Lys Cys Phe Gly Cys Gly Val Gly Gly Asp
          50             55             60
Ala Ile Lys Phe Val Ser Leu Tyr Glu Asp Ile Ser Tyr Phe Glu Ala
          65             70             75             80
Ala Leu Glu Leu Ala Lys Arg Tyr Gly Lys Lys Leu Asp Leu Glu Lys
          85             90             95
Ile Ser Lys Asp Glu Lys Val Tyr Val Ala Leu Asp Arg Val Cys Asp
          100            105            110

```

Sequence Listing R10901 Corrected.txt

```

Phe Tyr Arg Glu Ser Leu Leu Lys Asn Arg Glu Ala Ser Glu Tyr Val
 115                      120                      125

Lys Ser Arg Gly Ile Asp Pro Lys Val Ala Arg Lys Phe Asp Leu Gly
 130                      135                      140

Tyr Ala Pro Ser Ser Glu Ala Leu Val Lys Val Leu Lys Glu Asn Asp
 145                      150                      155                      160

Leu Leu Glu Ala Tyr Leu Glu Thr Lys Asn Leu Leu Ser Pro Thr Lys
 163                      170                      175

Gly Val Tyr Arg Asp Leu Phe Leu Arg Arg Val Val Ile Pro Ile Lys
 180                      185                      190

Asp Pro Arg Gly Arg Val Ile Gly Phe Gly Gly Arg Arg Ile Val Glu
 195                      200                      205

Asp Lys Ser Pro Lys Tyr Ile Asn Ser Pro Asp Ser Arg Val Phe Lys
 210                      215                      220

Lys Gly Glu Asn Leu Phe Gly Leu Tyr Glu Ala Lys Glu Tyr Ile Lys
 225                      230                      235                      240

Glu Glu Gly Phe Ala Ile Leu Val Glu Gly Tyr Phe Asp Leu Leu Arg
 245                      250                      255

Leu Phe Ser Glu Gly Ile Arg Asn Val Val Ala Pro Leu Gly Thr Ala
 260                      265                      270

Leu Thr Gln Asn Gln Ala Asn Leu Leu Ser Lys Phe Thr Lys Lys Val
 275                      280                      285

Tyr Ile Leu Tyr Asp Gly Asp Asp Ala Gly Arg Lys Ala Met Lys Ser
 290                      295                      300

Ala Ile Pro Leu Leu Leu Ser Ala Gly Val Glu Val Tyr Pro Val Tyr
 305                      310                      315                      320

Leu Pro Glu Gly Tyr Asp Pro Asp Glu Phe Ile Lys Glu Phe Gly Lys
 325                      330                      335

Glu Glu Leu Arg Arg Leu Ile Asn Ser Ser Gly Glu Leu Phe Glu Thr
 340                      345                      350

Leu Ile Lys Thr Ala Arg Glu Asn Leu Glu Glu Lys Thr Arg Glu Phe
 355                      360                      365

Arg Tyr Tyr Leu Gly Phe Ile Ser Asp Gly Val Arg Arg Phe Ala Leu
 370                      375                      380

Ala Ser Glu Phe His Thr Lys Tyr Lys Val Pro Met Glu Ile Leu Leu
 385                      390                      395                      400

Met Lys Ile Glu Lys Asn Ser Gln Glu Lys Glu Ile Lys Leu Ser Phe
 405                      410                      415

Lys Glu Lys Ile Phe Leu Lys Gly Leu Ile Glu Leu Lys Pro Lys Ile
 420                      425                      430

```

Sequence_Listing_R10901_Corrected.txt

Asp Leu Glu Val Leu Asn Leu Ser Pro Glu Leu Lys Glu Leu Ala Val
435 440 445

Asn Ala Leu Asn Gly Glu Glu His Leu Leu Pro Lys Glu Val Leu Glu
450 455 460

Tyr Gln Val Asp Asn Leu Glu Lys Leu Phe Asn Asn Ile Leu Arg Asp
465 470 475 480

Leu Gln Lys Ser Gly Lys Lys Arg Lys Lys Arg Gly Leu Lys Asn Val
485 490 495

Asn Thr

<210> 135

<211> 705

<212> DNA

<213> Aquifex aeolicus

<400> 135

atgcaagata cgcctacctg cagtatttgt caggggacgg gattcgtaaa gaccgaagac 60
aacaaggtaa ggctctgcga atgcaggttc aagaaaaggg atgtaaacag ggaactaaac 120
atcccaaaaga ggtactggaa cgccaaactta gacacttacc acccaaagaa cgtatccag 180
aacagggcac ttttagcatg aagggctctc gtccacaact tcaatcccga ggaagggaaa 240
gggcttaact ttgtaggatc tccctggagtc ggcaaaaacte accttgcggt tgcaacatta 300
aaagcgattt atgagaagaa ggaatcaga ggatacttct tcgatacaga ggaatcctaata 360
ttcagggttaa aacacttaat ggacgagggga aaggatacaa agtttttaaa aactgtctta 420
aactcacggt ttttggttct cgacgacctc ggttctgaga ggctcagtgga ctggcagagg 480
gaactcatct cttacataat cacttacagg tataacaacc ttaagagcac gataataacc 540
acgaattact cactccagag ggaagaagag agtagcgtga ggataagtcg gcatcttgca 600
agcagactcg gagaaaacgt agtttcaaaa atttacgaga tgaacgagtt gctcgttata 660
aagggttccg acctcaggaa gtctaaaaag gtatcaaccc catct 705

<210> 136

<211> 235

<212> PRT

<213> Aquifex aeolicus

<400> 136

Met Gln Asp Thr Ala Thr Cys Ser Ile Cys Gln Gly Thr Gly Phe Val
1 5 10 15

Lys Thr Glu Asp Asn Lys Val Arg Leu Cys Glu Cys Arg Phe Lys Lys
20 25 30

Arg Asp Val Asn Arg Glu Leu Asn Ile Pro Lys Arg Tyr Trp Asn Ala
35 40 45

Asn Leu Asp Thr Tyr His Pro Lys Asn Val Ser Gln Asn Arg Ala Leu
50 55 60

Leu Thr Ile Arg Val Phe Val His Asn Phe Asn Pro Glu Glu Gly Lys
65 70 75 80

Gly Lys Thr Phe Val Gly Ser Pro Gly Val Gly Lys Thr His Leu Ala

Sequence_Listing_R10901_Corrected.txt

85

90

95

```

Val Ala Thr Leu Lys Ala Ile Tyr Glu Lys Lys Gly Ile Arg Gly Tyr
      100      105      110

Phe Phe Asp Thr Lys Asp Leu Ile Phe Arg Leu Lys His Leu Met Asp
      115      120      125

Glu Gly Lys Asp Thr Lys Phe Leu Lys Thr Val Leu Asn Ser Pro Val
      130      135      140

Leu Val Leu Asp Asp Leu Gly Ser Glu Arg Leu Ser Asp Trp Gln Arg
      145      150      155      160

Glu Leu Ile Ser Tyr Ile Ile Thr Tyr Arg Tyr Asn Asn Leu Lys Ser
      165      170      175

Thr Ile Ile Thr Thr Asn Tyr Ser Leu Gln Arg Glu Glu Glu Ser Ser
      180      185      190

Val Arg Ile Ser Ala Asp Leu Ala Ser Arg Leu Gly Glu Asn Val Val
      195      200      205

Ser Lys Ile Tyr Glu Met Asn Glu Leu Leu Val Ile Lys Gly Ser Asp
      210      215      220

Leu Arg Lys Ser Lys Lys Leu Ser Thr Pro Ser
      225      230      235

<210> 137
<211> 4101
<212> DNA
<213> Thermatoga maritima

<400> 137
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gtgcgttttac tggagaagaa gacgcgggtt cgagtcacgc tgaacgggtg tcaaaaaagt 180
aacggggatc taaggggaaa gatactttcc ctcttcaacg gtaatgtgcc ttacataaaa 240
gatgttgttt tcgaaggaaa caggctgatt ctgaaaagtgc ttggagattt cgcgcgggac 300
aggatcgctt ccaaaactcag aagcacgaaa aaacagctcg atgaactgct gcctcccgga 360
acagagatca tgctggagggt tgtggagcct ccggaagatc ttttgaaaaa ggaagtacca 420
caaccagaaa agagagaaga accaaaagggt gaagaattga agatcgagga tgaaaaccac 480
atctttggac agaaaaccag aaagatcgct ttcacccctt caaaatctt tgagtacaac 540
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cttctcgaaa acgggggagcc caccctttac gtgaagggaa tcacaaaaact tcccgaaagc 780
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cccgcatgat ccttcacgga tcatgggaac gtccaggcca taccttacct ctacgcgcgc 960
gcgaanaaag ctggaataaa gccattttc ggatcgaaag cgtatctggt gagtgcagtg 1020
gagcccgctc taaggaaatc ctccgcagat tgcagctttg gagatgccac gtctgtctgc 1080
ctcgcattcg agacgacggg tctcgaccgg caggtggatg agatcatcga gataggagcg 1140
gtgaagatca aggtgtggcca gatagtggac gagtaccaca ctctcataaa gccttcacag 1200
gagatctcaa gaaaagttc ggagatcacc ggaatcactc aagagatgct gaaaaacaag 1260
agaagcatcg aggaagtctt gccggagttc ctccgttttc tggagattc catcatcgta 1320
gcacacaacg ccaacttcga ctacagattt ctgaggctgt ggatcaaaaa agtgcaggga 1380

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Sequence Listing R10901 Corrected.txt

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tcgctgagaa ttccgttcaa caaacttcca ggaactgggt acagcgttgc cgagtcgata 3960
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<210> 138

<211> 1367

<212> PRT

<213> *Thermatoga maritima*

<400> 138

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Leu Glu Ile Asp Pro Asp Ala Gly Val Val Leu Val Ser Val Glu Lys
20 25 30

Sequence_Listing_R10901_Corrected.txt

Phe Ser Glu Glu Ile Glu Asp Leu Val Arg Leu Leu Glu Lys Lys Thr
 35 40 45
 Arg Phe Arg Val Ile Val Asn Gly Val Gln Lys Ser Asn Gly Asp Leu
 50 55 60
 Arg Gly Lys Ile Leu Ser Leu Leu Asn Gly Asn Val Pro Tyr Ile Lys
 65 70 75 80
 Asp Val Val Phe Glu Gly Asn Arg Leu Ile Leu Lys Val Leu Gly Asp
 85 90 95
 Phe Ala Arg Asp Arg Ile Ala Ser Lys Leu Arg Ser Thr Lys Lys Gln
 100 105 110
 Leu Asp Glu Leu Leu Pro Pro Gly Thr Glu Ile Met Leu Glu Val Val
 115 120 125
 Glu Pro Pro Glu Asp Leu Leu Lys Lys Glu Val Pro Gln Pro Glu Lys
 130 135 140
 Arg Glu Glu Pro Lys Gly Glu Glu Leu Lys Ile Glu Asp Glu Asn His
 145 150 155 160
 Ile Phe Gly Gln Lys Pro Arg Lys Ile Val Phe Thr Pro Ser Lys Ile
 165 170 175
 Phe Glu Tyr Asn Lys Lys Thr Ser Val Lys Gly Lys Ile Phe Lys Ile
 180 185 190
 Glu Lys Ile Glu Gly Lys Arg Thr Val Leu Leu Ile Tyr Leu Thr Asp
 195 200 205
 Gly Glu Asp Ser Leu Ile Cys Lys Val Phe Asn Asp Val Glu Lys Val
 210 215 220
 Glu Gly Lys Val Ser Val Gly Asp Val Ile Val Ala Thr Gly Asp Leu
 225 230 235 240
 Leu Leu Glu Asn Gly Glu Pro Thr Leu Tyr Val Lys Gly Ile Thr Lys
 245 250 255
 Leu Pro Glu Ala Lys Arg Met Asp Lys Ser Pro Val Lys Arg Val Glu
 260 265 270
 Leu His Ala His Thr Lys Phe Ser Asp Gln Asp Ala Ile Thr Asp Val
 275 280 285
 Asn Glu Tyr Val Lys Arg Ala Lys Glu Trp Gly Phe Pro Ala Ile Ala
 290 295 300
 Leu Thr Asp His Gly Asn Val Gln Ala Ile Pro Tyr Phe Tyr Asp Ala
 305 310 315 320
 Ala Lys Glu Ala Gly Ile Lys Pro Ile Phe Gly Ile Glu Ala Tyr Leu
 325 330 335
 Val Ser Asp Val Glu Pro Val Ile Arg Asn Leu Ser Asp Asp Ser Thr

Sequence_Listing_R10901_Corrected.txt

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340                               345                               350
Phe Gly Asp Ala Thr Phe Val Val Leu Asp Phe Glu Thr Thr Gly Leu
355                               360                               365

Asp Pro Gln Val Asp Glu Ile Ile Glu Ile Gly Ala Val Lys Ile Gln
370                               375                               380

Gly Gly Gln Ile Val Asp Glu Tyr His Thr Leu Ile Lys Pro Ser Arg
385                               390                               395                               400

Glu Ile Ser Arg Lys Ser Ser Glu Ile Thr Gly Ile Thr Gln Glu Met
405                               410                               415

Leu Glu Asn Lys Arg Ser Ile Glu Glu Val Leu Pro Glu Phe Leu Gly
420                               425                               430

Phe Leu Glu Asp Ser Ile Ile Val Ala His Asn Ala Asn Phe Asp Tyr
435                               440                               445

Arg Phe Leu Arg Leu Trp Ile Lys Lys Val Met Gly Leu Asp Trp Glu
450                               455                               460

Arg Pro Tyr Ile Asp Thr Leu Ala Leu Ala Lys Ser Leu Leu Lys Leu
465                               470                               475                               480

Arg Ser Tyr Ser Leu Asp Ser Val Val Glu Lys Leu Gly Leu Gly Pro
485                               490                               495

Phe Arg His His Arg Ala Leu Asp Asp Ala Arg Val Thr Ala Gln Val
500                               505                               510

Phe Leu Arg Phe Val Glu Met Met Lys Lys Ile Gly Ile Thr Lys Leu
515                               520                               525

Ser Glu Met Glu Lys Leu Lys Asp Thr Ile Asp Tyr Thr Ala Leu Lys
530                               535                               540

Pro Phe His Cys Thr Ile Leu Val Gln Asn Lys Lys Gly Leu Lys Asn
545                               550                               555                               560

Leu Tyr Lys Leu Val Ser Asp Ser Tyr Ile Lys Tyr Phe Tyr Gly Val
565                               570                               575

Pro Arg Ile Leu Lys Ser Glu Leu Ile Glu Asn Arg Glu Gly Leu Leu
580                               585                               590

Val Gly Ser Ala Cys Ile Ser Gly Glu Leu Gly Arg Ala Ala Leu Glu
595                               600                               605

Gly Ala Ser Asp Ser Glu Leu Glu Glu Ile Ala Lys Phe Tyr Asp Tyr
610                               615                               620

Ile Glu Val Met Pro Leu Asp Val Ile Ala Glu Asp Glu Glu Asp Leu
625                               630                               635                               640

Asp Arg Glu Arg Leu Lys Glu Val Tyr Arg Lys Leu Tyr Arg Ile Ala
645                               650                               655

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Sequence Listing R10901_Corrected.txt

Lys Lys Leu Asn Lys Phe Val Val Met Thr Gly Asp Val His Phe Leu
660 665 670

Asp Pro Glu Asp Ala Arg Gly Arg Ala Ala Leu Leu Ala Pro Gln Gly
675 680 685

Asn Arg Asn Phe Glu Asn Gln Pro Ala Leu Tyr Leu Arg Thr Thr Glu
690 695 700

Glu Met Leu Glu Lys Ala Ile Glu Ile Phe Glu Asp Glu Glu Ile Ala
705 710 715 720

Arg Glu Val Val Ile Glu Asn Pro Asn Arg Ile Ala Asp Met Ile Glu
725 730 735

Glu Val Gln Pro Leu Glu Lys Lys Leu His Pro Pro Ile Ile Glu Asn
740 745 750

Ala Asp Glu Ile Val Arg Asn Leu Thr Met Lys Arg Ala Tyr Glu Ile
755 760 765

Tyr Gly Asp Pro Leu Pro Glu Ile Val Gln Lys Arg Val Glu Lys Glu
770 775 780

Leu Asn Ala Ile Ile Asn His Gly Tyr Ala Val Leu Tyr Leu Ile Ala
785 790 795 800

Gln Glu Leu Val Gln Lys Ser Met Ser Asp Gly Tyr Val Val Gly Ser
805 810 815

Arg Gly Ser Val Gly Ser Ser Leu Val Ala Asn Leu Leu Gly Ile Thr
820 825 830

Glu Val Asn Pro Leu Pro Pro His Tyr Arg Cys Pro Glu Cys Lys Tyr
835 840 845

Phe Glu Val Val Glu Asp Asp Arg Tyr Gly Ala Gly Tyr Asp Leu Pro
850 855 860

Asn Lys Asn Cys Pro Arg Cys Gly Ala Pro Leu Arg Lys Asp Gly His
865 870 875 880

Gly Ile Pro Phe Glu Thr Phe Met Gly Phe Glu Gly Asp Lys Val Pro
885 890 895

Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Glu Arg Ala His Arg
900 905 910

Phe Val Glu Glu Leu Phe Gly Lys Asp His Val Tyr Arg Ala Gly Thr
915 920 925

Ile Asn Thr Ile Ala Glu Arg Ser Ala Val Gly Tyr Val Arg Ser Tyr
930 935 940

Glu Glu Lys Thr Gly Lys Lys Leu Arg Lys Ala Glu Met Glu Arg Leu
945 950 955 960

Val Ser Met Ile Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro Gly
965 970 975

Sequence_Listing_R10901_Corrected.txt

Gly Leu Met Ile Ile Pro Lys Asp Lys Glu Val Tyr Asp Phe Thr Pro
980 985 990

Ile Gln Tyr Pro Ala Asn Asp Arg Asn Ala Gly Val Phe Thr Thr His
995 1000 1005

Phe Ala Tyr Glu Thr Ile His Asp Asp Leu Val Lys Ile Asp Ala Leu
1010 1015 1020

Gly His Asp Asp Pro Thr Phe Ile Lys Met Leu Lys Asp Leu Thr Gly
1025 1030 1035 1040

Ile Asp Pro Met Thr Ile Pro Met Asp Asp Pro Asp Thr Leu Ala Ile
1045 1050 1055

Phe Ser Ser Val Lys Pro Leu Gly Val Asp Pro Val Glu Leu Glu Ser
1060 1065 1070

Asp Val Gly Thr Tyr Gly Ile Pro Glu Phe Gly Thr Glu Phe Val Arg
1075 1080 1085

Gly Met Leu Val Glu Thr Arg Pro Lys Ser Phe Ala Glu Leu Val Arg
1090 1095 1100

Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Asn Asn Ala Arg
1105 1110 1115 1120

Asp Trp Ile Asn Leu Gly Tyr Ala Lys Leu Ser Glu Val Ile Ser Cys
1125 1130 1135

Arg Asp Asp Ile Met Asn Phe Leu Ile His Lys Gly Met Glu Pro Ser
1140 1145 1150

Leu Ala Phe Lys Ile Met Glu Asn Val Arg Lys Gly Lys Gly Ile Thr
1155 1160 1165

Glu Glu Met Glu Ser Glu Met Arg Arg Leu Lys Val Pro Glu Trp Phe
1170 1175 1180

Ile Glu Ser Cys Lys Arg Ile Lys Tyr Leu Phe Pro Lys Ala His Ala
1185 1190 1195 1200

Val Ala Tyr Val Ser Met Ala Phe Arg Ile Ala Tyr Phe Lys Val His
1205 1210 1215

Tyr Pro Leu Gln Phe Tyr Ala Ala Tyr Phe Thr Ile Lys Gly Asp Gln
1220 1225 1230

Phe Asp Pro Val Leu Val Leu Arg Gly Lys Glu Ala Ile Lys Arg Arg
1235 1240 1245

Leu Arg Glu Leu Lys Ala Met Pro Ala Lys Asp Ala Gln Lys Lys Asn
1250 1255 1260

Glu Val Ser Val Leu Glu Val Ala Leu Glu Met Ile Leu Arg Gly Phe
1265 1270 1275 1280

Ser Phe Leu Pro Pro Asp Ile Phe Lys Ser Asp Ala Lys Lys Phe Leu

Sequence_Listing_R10901_Corrected.txt

1285

1290

1295

Ile Glu Gly Asn Ser Leu Arg Ile Pro Phe Asn Lys Leu Pro Gly Leu
 1300 1305 1310

Gly Asp Ser Val Ala Glu Ser Ile Ile Arg Ala Arg Glu Glu Lys Pro
 1315 1320 1325

Phe Thr Ser Val Glu Asp Leu Met Lys Arg Thr Lys Val Asn Lys Asn
 1330 1335 1340

His Ile Glu Leu Met Lys Ser Leu Gly Val Leu Gly Asp Leu Pro Glu
 1345 1350 1355 1360

Thr Glu Gln Phe Thr Leu Phe
 1365

<210> 139

<211> 567

<212> DNA

<213> *Thermatoga maritima*

<400> 139

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 accgatccct ttgccggaga cgggatagtt gaaatagccg ctgttcctgt cttcaagggg 120
 aagatctaca gaacaaagc gtttcaactct ctctggaatc ccagaataag aatccctgcg 180
 ctgattcaga aagttcaagg tatcagcaac atggacatcg tgggaagcgc agacatggac 240
 acagtttacg atcttttcag ggattacgtg aagggaaacgg tgcctcgtgt tcacaacgcc 300
 aacttcgacc tcacttttct ggatatgatg gaaaaggaaa cgggaaactt tccaataaac 360
 aatccctaca tcgacacact cgatctttca gaagagatct ttggaaagcc tcattctctc 420
 aaatggctct ccgaagaact tggataaaaa accacgatac ggcacogtgc tcttcacgat 480
 gccctgggtga ccgcaagagt ttttgtgaag ctgtgtgaat ttcttggtga aaacagggtc 540
 aacgaattca tacgtggaaa acggggg 567

<210> 140

<211> 189

<212> PRT

<213> *Thermatoga maritima*

<400> 140

Met Leu Ala Met Ile Trp Asn Asp Thr Val Phe Cys Val Val Asp Thr
 1 5 10 15

Glu Thr Thr Gly Thr Asp Pro Phe Ala Gly Asp Arg Ile Val Glu Ile
 20 25 30

Ala Ala Val Pro Val Phe Lys Gly Lys Ile Tyr Arg Asn Lys Ala Phe
 35 40 45

His Ser Leu Val Asn Pro Arg Ile Arg Ile Pro Ala Leu Ile Gln Lys
 50 55 60

Val His Gly Ile Ser Asn Met Asp Ile Val Glu Ala Pro Asp Met Asp
 65 70 75 80

Thr Val Tyr Asp Leu Phe Arg Asp Tyr Val Lys Gly Thr Val Leu Val
 85 90 95

Sequence_Listing_R10901_Corrected.txt

Phe His Asn Ala Asn Phe Asp Leu Thr Phe Leu Asp Met Met Ala Lys
100 105 110

Glu Thr Gly Asn Phe Pro Ile Thr Asn Pro Tyr Ile Asp Thr Leu Asp
115 120 125

Leu Ser Glu Glu Ile Phe Gly Arg Pro His Ser Leu Lys Trp Leu Ser
130 135 140

Glu Arg Leu Gly Ile Lys Thr Thr Ile Arg His Arg Ala Leu Pro Asp
145 150 155 160

Ala Leu Val Thr Ala Arg Val Phe Val Lys Leu Val Glu Phe Leu Gly
165 170 175

Glu Asn Arg Val Asn Glu Phe Ile Arg Gly Lys Arg Gly
180 185

<210> 141

<211> 1434

<212> DNA

<213> *Thermatoga maritima*

<400> 141

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<210> 142

<211> 478

<212> PRT

<213> *Thermatoga maritima*

<400> 142

Met Glu Val Leu Tyr Arg Lys Tyr Arg Pro Lys Thr Ser Glu Val

Sequence_Listing_R10901_Corrected.txt

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1           5           10          15
Val Asn Gln Asp His Val Lys Lys Ala Ile Ile Gly Ala Ile Gln Lys
      20              25              30
Asn Ser Val Ala His Gly Tyr Ile Phe Ala Gly Pro Arg Gly Thr Gly
      35              40              45
Lys Thr Thr Leu Ala Arg Ile Leu Ala Lys Ser Leu Asn Cys Glu Asn
      50              55              60
Arg Lys Gly Val Glu Pro Cys Asn Ser Cys Arg Ala Cys Arg Glu Ile
      65              70              75              80
Asp Glu Gly Thr Phe Met Asp Val Ile Glu Leu Asp Ala Ala Ser Asn
      85              90              95
Arg Gly Ile Asp Glu Ile Arg Arg Ile Arg Asp Ala Val Gly Tyr Arg
      100             105             110
Pro Met Glu Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Val His Met
      115             120             125
Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro
      130             135             140
Pro Ser His Val Val Phe Val Leu Ala Thr Thr Asn Leu Glu Lys Val
      145             150             155             160
Pro Pro Thr Ile Ile Ser Arg Cys Gln Val Phe Glu Phe Arg Asn Ile
      165             170             175
Pro Asp Glu Leu Ile Glu Lys Arg Leu Gln Glu Val Ala Glu Ala Glu
      180             185             190
Gly Ile Glu Ile Asp Arg Glu Ala Leu Ser Phe Ile Ala Lys Arg Ala
      195             200             205
Ser Gly Gly Leu Arg Asp Ala Leu Thr Met Leu Glu Gln Val Trp Lys
      210             215             220
Phe Ser Glu Gly Lys Ile Asp Leu Glu Thr Val His Arg Ala Leu Gly
      225             230             235             240
Leu Ile Pro Ile Gln Val Val Arg Asp Tyr Val Asn Ala Ile Phe Ser
      245             250             255
Gly Asp Val Lys Arg Val Phe Thr Val Leu Asp Asp Val Tyr Tyr Ser
      260             265             270
Gly Lys Asp Tyr Glu Val Leu Ile Gln Glu Ala Val Glu Asp Leu Val
      275             280             285
Glu Asp Leu Glu Arg Glu Arg Gly Val Tyr Gln Val Ser Ala Asn Asp
      290             295             300
Ile Val Gln Val Ser Arg Gln Leu Leu Asn Leu Leu Arg Glu Ile Lys
      305             310             315             320

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Sequence_Listing_R10901_Corrected.txt

Phe Ala Glu Glu Lys Arg Leu Val Cys Lys Val Gly Ser Ala Tyr Ile
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Ala Thr Arg Phe Ser Thr Thr Asn Val Gln Glu Asn Asp Val Arg Glu
340 345 350

Lys Asn Asp Asn Ser Asn Val Gln Gln Lys Glu Glu Lys Lys Glu Thr
355 360 365

Val Lys Ala Lys Glu Glu Lys Gln Glu Asp Ser Glu Phe Glu Lys Arg
370 375 380

Phe Lys Glu Leu Met Glu Glu Leu Lys Glu Lys Gly Asp Leu Ser Ile
385 390 395 400

Phe Val Ala Leu Ser Leu Ser Glu Val Gln Phe Asp Gly Glu Lys Val
405 410 415

Ile Ile Ser Phe Asp Ser Ser Lys Ala Met His Tyr Glu Leu Met Lys
420 425 430

Lys Lys Leu Pro Glu Leu Glu Asn Ile Phe Ser Arg Lys Leu Gly Lys
435 440 445

Lys Val Glu Val Glu Leu Arg Leu Met Gly Lys Glu Glu Thr Ile Glu
450 455 460

Lys Val Ser Gln Lys Ile Leu Arg Leu Phe Glu Gln Glu Gly
465 470 475

<210> 143

<211> 1098

<212> DNA

<213> *Thermatoga maritima*

<400> 143

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aatctctaca tctgcgcgac cgatctcgag accggagtca aagcaaccgt gaatgccgct 180
gaaatctccg gtgaggcacg ttttgtggta ccaggagatg tcattcagaa gatggccaag 240
gttctccag atgagataac ggaactttct tttagagggg atgctcttgt tataagttct 300
ggaagcaccc ttttcaggat caccaccatg ccgcggagc aattccaga gataacgcct 360
gccgagttcg gaataacctt cgaagttgac acttcgctcc tcgaggaagt ggttgaaaag 420
gtcatcttcg ccgctgccaa agacgagttc atgcgaaatc tgaatggagt tttctgggaa 480
ctccacaaga atcttctcag gctggttgca agtgatgggt tcagacttgc acttgctgaa 540
gagcagatag aaaaacgagg agaggcgagt tttctgctct ctttgaagag catgaaagaa 600
gttcaaaaag tgctggacaa cacaacggag ccgactataa cgggtgagga cgaatgaa 660
agggtttctc tgcgacaaa tgatgtagaa accgtgatga gagtggtcga cgtgtaatt 720
cccgattaca aaagggtgat ccccgaaact tcaaaaaaga aagtgggtgt ttccagaaaa 780
gaactcaggg aatctttgaa gaggggtgat gtgattgcca gcaagggaag cgagtccgtg 840
aagttcgaaa tagaagaaaa cgttatgaga ctgtgagca agagcccgga ttatggagaa 900
gtggtcgatg aagttgaagt tcaaaaaaga ggggaagatc tcgtgatcgc ttccaacccg 960
aagttcatcg aggacgtttt gaagcacatt gagactgaag aaatcgaagt gaacttcgtt 1020
gattctacca gtccatgtca gataaatcca ctcgatattt ctggatacct ttacatagt 1080
atgcccatca gactggca
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<210> 144

Sequence_Listing_R10901_Corrected.txt

<211> 366

<212> PRT

<213> *Thermatoga maritima*

<400> 144

Met Lys Val Thr Val Thr Leu Glu Leu Lys Asp Lys Ile Thr Ile
1 5 10 15

Ala Ser Lys Ala Leu Ala Lys Lys Ser Val Lys Pro Ile Leu Ala Gly
20 25 30

Phe Leu Phe Glu Val Lys Asp Gly Asn Phe Tyr Ile Cys Ala Thr Asp
35 40 45

Leu Glu Thr Gly Val Lys Ala Thr Val Asn Ala Ala Glu Ile Ser Gly
50 55 60

Glu Ala Arg Phe Val Val Pro Gly Asp Val Ile Gln Lys Met Val Lys
65 70 75 80

Val Leu Pro Asp Glu Ile Thr Glu Leu Ser Leu Glu Gly Asp Ala Leu
85 90 95

Val Ile Ser Ser Gly Ser Thr Val Phe Arg Ile Thr Thr Met Pro Ala
100 105 110

Asp Glu Phe Pro Glu Ile Thr Pro Ala Glu Ser Gly Ile Thr Phe Glu
115 120 125

Val Asp Thr Ser Leu Leu Glu Glu Met Val Glu Lys Val Ile Phe Ala
130 135 140

Ala Ala Lys Asp Glu Phe Met Arg Asn Leu Asn Gly Val Phe Trp Glu
145 150 155 160

Leu His Lys Asn Leu Leu Arg Leu Val Ala Ser Asp Gly Phe Arg Leu
165 170 175

Ala Leu Ala Glu Gln Ile Glu Asn Glu Glu Glu Ala Ser Phe Leu
180 185 190

Leu Ser Leu Lys Ser Met Lys Glu Val Gln Asn Val Leu Asp Asn Thr
195 200 205

Thr Glu Pro Thr Ile Thr Val Arg Tyr Asp Gly Arg Arg Val Ser Leu
210 215 220

Ser Thr Asn Asp Val Glu Thr Val Met Arg Val Val Asp Ala Glu Phe
225 230 235 240

Pro Asp Tyr Lys Arg Val Ile Pro Glu Thr Phe Lys Thr Lys Val Val
245 250 255

Val Ser Arg Lys Glu Leu Arg Glu Ser Leu Lys Arg Val Met Val Ile
260 265 270

Ala Ser Lys Gly Ser Glu Ser Val Lys Phe Glu Ile Glu Glu Asn Val
275 280 285

Sequence Listing R10901_Corrected.txt

Met Arg Leu Val Ser Lys Ser Pro Asp Tyr Gly Glu Val Val Asp Glu
290 295 300

Val Glu Val Gln Lys Glu Gly Glu Asp Leu Val Ile Ala Phe Asn Pro
305 310 315 320

Lys Phe Ile Glu Asp Val Leu Lys His Ile Glu Thr Glu Glu Ile Glu
325 330 335

Met Asn Phe Val Asp Ser Thr Ser Pro Cys Gln Ile Asn Pro Leu Asp
340 345 350

Ile Ser Gly Tyr Leu Tyr Ile Val Met Pro Ile Arg Leu Ala
355 360 365

<210> 145

<211> 972

<212> DNA

<213> *Thermatoga maritima*

<400> 145

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atgccagtcac cgtttctcac aggtactgca gaaactcaga aggaagaatt gataaagaaa 60
ctctcgaagg atggtaacgt ggagtacata aggatccatc cggaggatcc cgacaagatc 120
gatttcataa ggtctttact caggacaaag acgatctttt ccaacaagac gatcattgac 180
atcgtcaatt tcgatgagtg gaaagcacag gacgagaagc gtctcgttga acttttgaaa 240
aacgtacogg aagaacgtca tatcttcac cgtttcctaaa aaacaggtgg aaagggagta 300
gcgctggagc ttccgaagcc atgggaaaac gacaagtggc ttgagtggat agaaaagcgc 360
ttcagggaga atcgttttgc catcgataaa gatgccttcc agctgttttt ctccaaggtt 420
ggaacgaacg acctgatcat agaaaggagc attgaaaaac tgaagactta ttccgaggac 480
agaaagataa cgttagaaga cgtggaagag gtctgtttta cctatcacag tccgggatac 540
gatgatTTTT gotttgcgtg ttccgaagga aaaagggaagc tcgctcactc tcttctgtcg 600
cagctgtgga aaaccacaga gtccgtggtg attgccactg tccttgcgaa tcacttcttg 660
gatctcttca aaatcctcgt tcttgtgaca aagaaaagat actacacctg gcctgatgtg 720
tccaggggtg ccaagagcgt gggaattccc gtctcctgtg tggctcgttt cctcggttcc 780
tcttctaaga cctggaatt caaggtgatg aaccacctcc tctactacga tgtgaagaag 840
gttagaaaaga tactgagga tctctacgat ctggacagag ccgtgaaaag cgaagaagat 900
ccaaaacgct tcttcacaga gttcatagaa gaggtggcac tggatgtata ttctcttcag 960
agagatgaag aa 972
```

<210> 146

<211> 324

<212> PRT

<213> *Thermatoga maritima*

<400> 146

Met Pro Val Thr Phe Leu Thr Gly Thr Ala Glu Thr Gln Lys Glu Glu
1 5 10 15

Leu Ile Lys Lys Leu Leu Lys Asp Gly Asn Val Glu Tyr Ile Arg Ile
20 25 30

His Pro Glu Asp Pro Asp Lys Ile Asp Phe Ile Arg Ser Leu Leu Arg
35 40 45

Thr Lys Thr Ile Phe Ser Asn Lys Thr Ile Ile Asp Ile Val Asn Phe
50 55 60

Sequence Listing_R10901_Corrected.txt

```

Asp Glu Trp Lys Ala Gln Glu Gln Lys Arg Leu Val Glu Leu Leu Lys
65          70          75          80
Asn Val Pro Glu Asp Val His Ile Phe Ile Arg Ser Gln Lys Thr Gly
85          90          95
Gly Lys Gly Val Ala Leu Glu Leu Pro Lys Pro Trp Glu Thr Asp Lys
100         105         110
Trp Leu Glu Trp Ile Glu Lys Arg Phe Arg Glu Asn Gly Leu Leu Ile
115         120         125
Asp Lys Asp Ala Leu Gln Leu Phe Phe Ser Lys Val Gly Thr Asn Asp
130         135         140
Leu Ile Ile Glu Arg Glu Ile Glu Lys Leu Lys Ala Tyr Ser Glu Asp
145         150         155         160
Arg Lys Ile Thr Val Glu Asp Val Glu Glu Val Val Phe Thr Tyr Gln
165         170         175
Thr Pro Gly Tyr Asp Asp Phe Cys Phe Ala Val Ser Glu Gly Lys Arg
180         185         190
Lys Leu Ala His Ser Leu Leu Ser Gln Leu Trp Lys Thr Thr Glu Ser
195         200         205
Val Val Ile Ala Thr Val Leu Ala Asn His Phe Leu Asp Leu Phe Lys
210         215         220
Ile Leu Val Leu Val Thr Lys Lys Arg Tyr Tyr Thr Trp Pro Asp Val
225         230         235         240
Ser Arg Val Ser Lys Glu Leu Gly Ile Pro Val Pro Arg Val Ala Arg
245         250         255
Phe Leu Gly Phe Ser Phe Lys Thr Trp Lys Phe Lys Val Met Asn His
260         265         270
Leu Leu Tyr Tyr Asp Val Lys Lys Val Arg Lys Ile Leu Arg Asp Leu
275         280         285
Tyr Asp Leu Asp Arg Ala Val Lys Ser Glu Glu Asp Pro Lys Pro Phe
290         295         300
Phe His Glu Phe Ile Glu Glu Val Ala Leu Asp Val Tyr Ser Leu Gln
305         310         315         320
Arg Asp Glu Glu

```

<210> 147

<211> 936

<212> DNA

<213> *Thermatoga maritima*

<400> 147

atgaacgatt tgatcagaaa gtacgctaaa gatcaactgg aaactttgaa aaggatcata 60

Sequence Listing_R10901_Corrected.txt

```

gaaaagtctg aaggaatatc catcctcata aatggagaag atctctcgta tccgagagaa 120
gtatcccttg aacttccoga gtacgtggag aaatttcccc cgaaggccctc ggaagtcttg 180
gagatagatc ccgaggggga gaacatagga atagaacgaca tcagaacgat aaaggacttc 240
ctgaactaca gccccgagct ctacacgaga aagtaacgtga tagtccacga ctgtgaaaga 300
atgacccagc aggcggcgaa cgggtttctg aaggcccttg aagaaccacc agaatacgtc 360
gtgatcgctt tgaacactcg ccgctggcat tatctactgc cgaagataaa gagccgagtg 420
ttcagagtgg ttgtgaacgt tccaaaggag ttcagagatc tcgtgaaaga gaaaatagga 480
gatctctggg aggaactctc acttcttgag agagacttca aaacggctct cgaagcctac 540
aaactctggg cggaaaaaact tctcggattg atggaaaagtc tcaaagtttt ggagacggaa 600
aaactcttga aaaaaggtcct tcaaaaaggg ctogaaggtt atctcgcgat tagggagctc 660
ctggagagat ttccaaggtt ggaatcgaag gaattctttg cgtcttttga tcaagtgact 720
aacacgataa caggaaaaag cgcgtttctt ttgatccaga gactgacaag aatcattctc 780
cacgaaaaaca catgggaaag cgttgaagat caaaaaagcg tgtctttctc cgattcaatt 840
ctcagggtga agatagcgaa tctgaacac aactcactc tgatgaacat cctcgcgata 900
cacagagaga gaaaagagag ttgtcaacgct tggagc 936

```

<210> 148

<211> 312

<212> PRT

<213> *Thermatoga maritima*

<400> 148

```

Met Asn Asp Leu Ile Arg Lys Tyr Ala Lys Asp Gln Leu Glu Thr Leu
  1             5             10            15

```

```

Lys Arg Ile Ile Glu Lys Ser Glu Gly Ile Ser Ile Leu Ile Asn Gly
      20             25            30

```

```

Glu Asp Leu Ser Tyr Pro Arg Glu Val Ser Leu Glu Leu Pro Glu Tyr
      35             40            45

```

```

Val Glu Lys Phe Pro Pro Lys Ala Ser Asp Val Leu Glu Ile Asp Pro
      50             55            60

```

```

Glu Gly Glu Asn Ile Gly Ile Asp Asp Ile Arg Thr Ile Lys Asp Phe
      65             70            75            80

```

```

Leu Asn Tyr Ser Pro Glu Leu Tyr Thr Arg Lys Tyr Val Ile Val His
      85             90            95

```

```

Asp Cys Glu Arg Glu Met Thr Gln Gln Ala Ala Asn Ala Phe Leu Lys Ala
     100            105            110

```

```

Leu Glu Glu Pro Pro Glu Tyr Ala Val Ile Val Leu Asn Thr Arg Arg
     115            120            125

```

```

Trp His Tyr Leu Leu Pro Thr Ile Lys Ser Arg Val Phe Arg Val Val
     130            135            140

```

```

Val Asn Val Pro Lys Glu Phe Arg Asp Leu Val Lys Glu Lys Ile Gly
     145            150            155            160

```

```

Asp Leu Trp Glu Glu Leu Pro Leu Leu Glu Arg Asp Phe Lys Thr Ala
     165            170            175

```

```

Leu Glu Ala Tyr Lys Leu Gly Ala Glu Lys Leu Ser Gly Leu Met Glu
     180            185            190

```

Sequence_Listing_R10901_Corrected.txt

```

Ser Leu Lys Val Leu Glu Thr Glu Lys Leu Leu Lys Lys Val Leu Ser
  195                                205

Lys Gly Leu Glu Gly Tyr Leu Ala Cys Arg Glu Leu Leu Glu Arg Phe
  210                                220

Ser Lys Val Glu Ser Lys Glu Phe Phe Ala Leu Phe Asp Gln Val Thr
  225                                235

Asn Thr Ile Thr Gly Lys Asp Ala Phe Leu Leu Ile Gln Arg Leu Thr
  245                                255

Arg Ile Ile Leu His Glu Asn Thr Trp Glu Ser Val Glu Asp Gln Lys
  260                                270

Ser Val Ser Phe Leu Asp Ser Ile Leu Arg Val Lys Ile Ala Asn Leu
  275                                285

Asn Asn Lys Leu Thr Leu Met Asn Ile Leu Ala Ile His Arg Glu Arg
  290                                300

Lys Arg Gly Val Asn Ala Trp Ser
  305                                310

```

```

<210> 149
<211> 423
<212> DNA
<213> Thermatoga maritima

```

```

<400> 149
atgtctttct tcaacaagat catactcata ggaagactcg tgagagatcc cgaagagaga 60
tacacgctca gcggaactcc agtcaccacc ttoaccatag cggtggacag gggtcccca 120
aagaacgcgc cggacgacgc tcaaacgact gatctcttca ggatcgctac ctttggaaga 180
ctggcagagt tgcctagaac ctatctcacc aaaggaaagg tcgtctctgt cgaaggtgaa 240
atgagaatga gaagatggga aacaccocact ggagaaaaga gggtatctcc gaaggtgtgc 300
gcaaacgctg ttgatctcat ggacagaaaa cctgctgaaa cagttagcga gactgaagag 360
gagctggaaa taccggaaga agacttttcc agcgatacct tcagtgaaga tgaaccacca 420
ttt

```

```

<210> 150
<211> 141
<212> PRT
<213> Thermatoga maritima

```

```

<400> 150
Met Ser Phe Phe Asn Lys Ile Ile Leu Ile Gly Arg Leu Val Arg Asp
  1           5           10          15

Pro Glu Glu Arg Tyr Thr Leu Ser Gly Thr Pro Val Thr Thr Phe Thr
  20           25           30

Ile Ala Val Asp Arg Val Pro Arg Lys Asn Ala Pro Asp Asp Ala Gln
  35           40           45

Thr Thr Asp Phe Phe Arg Ile Val Thr Phe Gly Arg Leu Ala Glu Phe
  50           55           60

```

Sequence_Listing_R10901_Corrected.txt

Ala Arg Thr Tyr Leu Thr Lys Gly Arg Leu Val Leu Val Glu Gly Glu
65 70 75 80

Met Arg Met Arg Arg Trp Glu Thr Pro Thr Gly Glu Lys Arg Val Ser
85 90 95

Pro Glu Val Val Ala Asn Val Val Arg Phe Met Asp Arg Lys Pro Ala
100 105 110

Glu Thr Val Ser Glu Thr Glu Glu Glu Leu Glu Ile Pro Glu Glu Asp
115 120 125

Phe Ser Ser Asp Thr Phe Ser Glu Asp Glu Pro Pro Phe
130 135 140

<210> 151

<211> 1353

<212> DNA

<213> *Thermatoga maritima*

<400> 151

atgcggtgttc ccccgacaaa cttagaggcc gaagttgctg tgctcggaag catattgata 60
gatccgctgg taataaaacga cgtttctgaa attttgagcc acgaagattt ctatctgaaa 120
aaacaccaa acatcttcag agcgatggaa gagctttacg acgaaggaaa accggtggag 180
gtggtttccg tctgtgacaa gcttcaaaagc atgggaaaac tcgagggaagt aggtggagat 240
ctggaagtgg cccagctcgc tgaggctgtg cccagttctg cacacgcact tcaactacgc 300
gagatcgtca aggaaaaaatc cattctgagg aaactcattg agatctccag aaaaatctca 360
gaaagtgcct acatggaaga agatgtggag atcctgctcg acaacgcaga aaagatgatc 420
ttcgagatct cagagatgaa aacgacaaaa tctacgatac atctgagagg catcatgcac 480
cgggtgtttg aaaaacctgga gaacttcagg gaaagagcca accttataga acccggtgtg 540
ctcataacgg gactaccaac gggattcaaa agtctggaca aacagacac acgggttccac 600
agctccgatac tgggtataat agcagcgaga cctccatgg gaaaaacctc ctctgcactc 660
tcaatagcga ggaacatggc tgtcaatttc gaaatccccg tcggaatat cagtctcgag 720
atgtccaaag aacagctcgc tcaaaagacta ctacgcatgg agtccggtgt ggatctttac 780
agcatcagaa caggatacct ggatcaggag aagtgggaaa gactcacaat agcggttctt 840
aaactctaca aagcacccat agttgtggac gatgagtcac tctctgatcc gcgacgttg 900
agggcaaaag cgagaaggat gaaaaaagaa tacgatglaa aagccatttt tctcgactat 960
ctccagctca tgcacctgaa aggaagaaaa gaaagcagac agcaggagat atccgagatc 1020
tcgagatctc tgaagctcct tgcgagggaa ctcgacatag tggtagatgc gctttcacag 1080
ctttcgaggg ccgtagaaca gagagaagac aaaaagacga ggcctgagtg cctcagggaa 1140
tccggtgcga tagaacagga cgcagacaca gtcatcttca tctacaggga ggaatatatt 1200
agggacaaaa aatccaaaga ggaagcaag ctctacgaac ctcaacgaagc tgaatatata 1260
atagtgaaac agagaaacgg tcccggttga acgatcactc tgatcttcga ccccgaaacg 1320
gttacgttcc atgaagtcca tgtggtgcat tca 1353

<210> 152

<211> 451

<212> PRT

<213> *Thermatoga maritima*

<400> 152

Met Arg Val Pro Pro His Asn Leu Glu Ala Glu Val Ala Val Leu Gly
1 5 10 15

Ser Ile Leu Ile Asp Pro Ser Val Ile Asn Asp Val Leu Glu Ile Leu
20 25 30

Sequence_Listing_R10901_Corrected.txt

```

Ser His Glu Asp Phe Tyr Leu Lys Lys His Gln His Ile Phe Arg Ala
    35                                40                                45

Met Glu Glu Leu Tyr Asp Glu Gly Lys Pro Val Asp Val Val Ser Val
    50                                55                                60

Cys Asp Lys Leu Gln Ser Met Gly Lys Leu Glu Val Gly Gly Asp
    65                                70                                75                                80

Leu Glu Val Ala Gln Leu Ala Glu Ala Val Pro Ser Ser Ala His Ala
    85                                90                                95

Leu His Tyr Ala Glu Ile Val Lys Glu Lys Ser Ile Leu Arg Lys Leu
    100                               105                               110

Ile Glu Ile Ser Arg Lys Ile Ser Glu Ser Ala Tyr Met Glu Glu Asp
    115                               120                               125

Val Glu Ile Leu Leu Asp Asn Ala Glu Lys Met Ile Phe Glu Ile Ser
    130                               135                               140

Glu Met Lys Thr Thr Lys Ser Tyr Asp His Leu Arg Gly Ile Met His
    145                               150                               155                               160

Arg Val Phe Glu Asn Leu Glu Asn Phe Arg Glu Arg Ala Asn Leu Ile
    165                               170                               175

Glu Pro Gly Val Leu Ile Thr Gly Leu Pro Thr Gly Phe Lys Ser Leu
    180                               185                               190

Asp Lys Gln Thr Thr Gly Phe His Ser Ser Asp Leu Val Ile Ile Ala
    195                               200                               205

Ala Arg Pro Ser Met Gly Lys Thr Ser Phe Ala Leu Ser Ile Ala Arg
    210                               215                               220

Asn Met Ala Val Asn Phe Glu Ile Pro Val Gly Ile Phe Ser Leu Glu
    225                               230                               235                               240

Met Ser Lys Glu Gln Leu Ala Gln Arg Leu Leu Ser Met Glu Ser Gly
    245                               250                               255

Val Asp Leu Tyr Ser Ile Arg Thr Gly Tyr Leu Asp Gln Glu Lys Trp
    260                               265                               270

Glu Arg Leu Thr Ile Ala Ala Ser Lys Leu Tyr Lys Ala Pro Ile Val
    275                               280                               285

Val Asp Asp Glu Ser Leu Leu Asp Pro Arg Ser Leu Arg Ala Lys Ala
    290                               295                               300

Arg Arg Met Lys Lys Glu Tyr Asp Val Lys Ala Ile Phe Val Asp Tyr
    305                               310                               315                               320

Leu Gln Leu Met His Leu Lys Gly Arg Lys Glu Ser Arg Gln Gln Glu
    325                               330                               335

Ile Ser Glu Ile Ser Arg Ser Leu Lys Leu Leu Ala Arg Glu Leu Asp

```

Sequence_Listing_R10901_Corrected.txt

340

345

350

Ile Val Val Ile Ala Leu Ser Gln Leu Ser Arg Ala Val Glu Gln Arg
 355 360 365

Glu Asp Lys Arg Pro Arg Leu Ser Asp Leu Arg Glu Ser Gly Ala Ile
 370 375 380

Glu Gln Asp Ala Asp Thr Val Ile Phe Ile Tyr Arg Glu Glu Tyr Tyr
 385 390 395 400

Arg Ser Lys Lys Ser Lys Glu Glu Ser Lys Leu His Glu Pro His Glu
 405 410 415

Ala Glu Ile Ile Ile Gly Lys Gln Arg Asn Gly Pro Val Gly Thr Ile
 420 425 430

Thr Leu Ile Phe Asp Pro Arg Thr Val Thr Phe His Glu Val Asp Val
 435 440 445

Val His Ser
 450

<210> 153

<211> 1695

<212> DNA

<213> *Thermatoga maritima*

<400> 153

```

gtgattcttc gagaggtcat cgaggaaata aaagaaaagg ttgacatcgt agaggtcatt 60
tcogagtacg tgaattottac ccgggttaggt tctctctaca gggctctctg tccctttcat 120
tcagaaacca atccttctctt ctacgttcat ccgggtttga agatatacca ttgtttcggc 180
tgcggtcgga gtggagagcgt catcaaatctt ctccaagaaa tggaaaggat cagtttccag 240
gaagcgctgg aaagacttgc caaaagagct gggattgac ttctctctca cagaacagaa 300
gggactttctg aatacggaaa atacattcgt ttgtacgaag aaacgtggaa aaggtacgtc 360
aaagagctgg agaatcgaa agaggcaaaa gactatttaa aaagcagagg ctctctgaa 420
gaagatatag caaagttcgg ctttgggtac gtccccaaga gatccagcat ctctatagaa 480
gttcagaaag gcatgaacat aacactggaa gaactgttca gatccggtat cgcgctgaaa 540
aagggtgacg gattcgttga tagatttcgaa ggaagaatcg ttgttccaat aaagaacgac 600
agtggtcata ttgtggcttt tgggtggcgt gctctcgcca acgaagaacc gaagtatttg 660
aactctccag agaccaggtt ttttctgaag aagaagacc ttctctctt cgaatgaggcg 720
aaaaaagtgg caaaagaggt tggtttttct gtoatcaccc aaggctactt cgacgcgctc 780
gcattcagaa aggatggaat accaacggcg gtgcgtgttc ttggggcgag tctttcaaga 840
gaggcgatct taaaactttc ggcgtattcg aaaaacgtca tactgtgttt cgataatgac 900
aaagcaggct tcagagccac tctcaaatcc ctocaggatc tcttagacta cgaattcaac 960
gtgcttctgg caaccccttc tctttacaaa gaccagatg aactctttca gaaagaagga 1020
gaaggttcat tgaaaaagat gctgaaaaac tcgcttctgt tgaataattt ctggtgacg 1080
gctggtgagg tcttctttga caggaaacgc ccgcggggtg tgaatccta cctttctttc 1140
ctcaaatggt ggggtccaaa gatgagaagg aaaggatatt tgaaacacat agaaaaatctc 1200
gtgaatgatt ttcatcttct tctccagata ccagaaaacc agattttgaa ctttttgaa 1260
aggcagaggt ctacactact gcctgttcat gagaccaagt cgtcaaaagt ttacgatgag 1320
ggagagagac ttgcttattt gtttttgaa tcagaggatt tgaggggaaa tgatttgaa 1380
ctggacttag aggtactcga agataaaaac gcgagggagt ttttcaagag agtctcactg 1440
ggagaagatt tgaacaaact catagaaaac ttcccaaaa agctgaaaag ctggaatttt 1500
gagacaattg aaagcattcc tcttccaaag gatcccgaga aattctctcg tgacctctcc 1560
gaaaagttga aaatccgcgc gatagagaga cgtatcgcat aaatagatga tatgataaag 1620
aaagcttcaa acgatgaaga aaggcgctctt ctctctctca tgaagtgga tctctctaga 1680
aaaaaaaga ggagg

```

Sequence_Listing_R10901_Corrected.txt

<210> 154

<211> 565

<212> PRT

<213> *Thermatoga maritima*

<400> 154

Met Ile Pro Arg Glu Val Ile Glu Glu Ile Lys Glu Lys Val Asp Ile
1 5 10 15Val Glu Val Ile Ser Glu Tyr Val Asn Leu Thr Arg Val Gly Ser Ser
20 25 30Tyr Arg Ala Leu Cys Pro Phe His Ser Glu Thr Asn Pro Ser Phe Tyr
35 40 45Val His Pro Gly Leu Lys Ile Tyr His Cys Phe Gly Cys Gly Ala Ser
50 55 60Gly Asp Val Ile Lys Phe Leu Gln Glu Met Glu Gly Ile Ser Phe Gln
65 70 75 80Glu Ala Leu Glu Arg Leu Ala Lys Arg Ala Gly Ile Asp Leu Ser Leu
85 90 95Tyr Arg Thr Glu Gly Thr Ser Glu Tyr Gly Lys Tyr Ile Arg Leu Tyr
100 105 110Glu Glu Thr Trp Lys Arg Tyr Val Lys Glu Leu Glu Lys Ser Lys Glu
115 120 125Ala Lys Asp Tyr Leu Lys Ser Arg Gly Phe Ser Glu Glu Asp Ile Ala
130 135 140Lys Phe Gly Phe Gly Tyr Val Pro Lys Arg Ser Ser Ile Ser Ile Glu
145 150 155 160Val Ala Glu Gly Met Asn Ile Thr Leu Glu Glu Leu Val Arg Tyr Gly
165 170 175Ile Ala Leu Lys Lys Gly Asp Arg Phe Val Asp Arg Phe Glu Gly Arg
180 185 190Ile Val Val Pro Ile Lys Asn Asp Ser Gly His Ile Val Ala Phe Gly
195 200 205Gly Arg Ala Leu Gly Asn Glu Glu Pro Lys Tyr Leu Asn Ser Pro Glu
210 215 220Thr Arg Tyr Phe Ser Lys Lys Lys Thr Leu Phe Leu Phe Asp Glu Ala
225 230 235 240Lys Lys Val Ala Lys Glu Val Gly Phe Phe Val Ile Thr Glu Gly Tyr
245 250 255Phe Asp Ala Leu Ala Phe Arg Lys Asp Gly Ile Pro Thr Ala Val Ala
260 265 270

Sequence Listing R10901 Corrected.txt

Val Leu Gly Ala Ser Leu Ser Arg Glu Ala Ile Leu Lys Leu Ser Ala
 275 280
 Tyr Ser Lys Asn Val Ile Leu Cys Phe Asp Asn Asp Lys Ala Gly Phe
 290 295 300
 Arg Ala Thr Leu Lys Ser Leu Glu Asp Leu Leu Asp Tyr Glu Phe Asn
 305 310 315 320
 Val Leu Val Ala Thr Pro Ser Pro Tyr Lys Asp Pro Asp Glu Leu Phe
 325 330 335
 Gln Lys Glu Gly Glu Gly Ser Leu Lys Lys Met Leu Lys Asn Ser Arg
 340 345 350
 Ser Phe Glu Tyr Phe Leu Val Thr Ala Gly Glu Val Phe Phe Asp Arg
 355 360 365
 Asn Ser Pro Ala Gly Val Arg Ser Tyr Leu Ser Phe Leu Lys Gly Trp
 370 375 380
 Val Gln Lys Met Arg Arg Lys Gly Tyr Leu Lys His Ile Glu Asn Leu
 385 390 395 400
 Val Asn Glu Val Ser Ser Ser Leu Gln Ile Pro Glu Asn Gln Ile Leu
 405 410 415
 Asn Phe Phe Glu Ser Asp Arg Ser Asn Thr Met Pro Val His Glu Thr
 420 425 430
 Lys Ser Ser Lys Val Tyr Asp Glu Gly Arg Gly Leu Ala Tyr Leu Phe
 435 440 445
 Leu Asn Tyr Glu Asp Leu Arg Glu Lys Ile Leu Glu Leu Asp Leu Glu
 450 455 460
 Val Leu Glu Asp Lys Asn Ala Arg Glu Phe Phe Lys Arg Val Ser Leu
 465 470 475 480
 Gly Glu Asp Leu Asn Lys Val Ile Glu Asn Phe Pro Lys Glu Leu Lys
 485 490 495
 Asp Trp Ile Phe Glu Thr Ile Glu Ser Ile Pro Pro Pro Lys Asp Pro
 500 505 510
 Glu Lys Phe Leu Gly Asp Leu Ser Glu Lys Leu Lys Ile Arg Arg Ile
 515 520 525
 Glu Arg Arg Ile Ala Glu Ile Asp Asp Met Ile Lys Lys Ala Ser Asn
 530 535 540
 Asp Glu Glu Arg Arg Leu Leu Ser Met Lys Val Asp Leu Leu Arg
 545 550 555 560
 Lys Ile Lys Arg Arg
 565

<210> 155

Sequence_Listing_R10901_Corrected.txt

<211> 804

<212> DNA

<213> Thermus thermophilus

<400> 155

```

atgggtcttac acccggtctca ccttggggca ataatcgggc acgaggccgt tctgcgcctc 60
cttccccgcc tcaccgccca gacctgctc ttctccggcc cagagggggg ggggcggcgc 120
accgtggccc gctggtaacg ctgggggctc aaccgcggtc tccccccgcc ctccctgggg 180
gagcaccggg acgtctctga ggtggggccc aaggcccggg acctccgggg cggggccgag 240
gtgcggcttg aggaggtggc gccctctttg gagtgggtgt ccagccaccc ccgggagcgg 300
gtgaaggttg ccattcttga ctggcccccac ctctcaccg aggcgcgcgc caacgcctc 360
ctcaagctcc tggaggagcc ccttctctac gccgcctcg tctctatcgc cccaagccgc 420
gccaccctcc tccccaccct ggcctcccg gccacggagg tggcattcgc ccccgtagcc 480
gaggaggccc tgcgcgcct caccacggac ccggagctcc tccgtacgc gcgcggggcc 540
ccgggcgcgc tcttagggc cctccaggac ccggaggggt accgggcccgc catggccagg 600
gcgcaagggg tcttgaagg ccgcgccctg gacgcctcg ctttgccttg ggagctttg 660
gccgaggagg aggggggtcc cgcctccac gccgtcctaa agcgcgcgga gcacctcctt 720
gccttgagc gggcgcgga ggcctggag gggtagctga gcccagact ggtcctcgcc 780
cggtggcct tagacttaga gaca                                     804

```

<210> 156

<211> 268

<212> PRT

<213> Thermus thermophilus

<400> 156

```

Met Ala Leu His Pro Ala His Pro Gly Ala Ile Ile Gly His Glu Ala
 1             5             10             15
Val Leu Ala Leu Leu Pro Arg Leu Thr Ala Gln Thr Leu Leu Phe Ser
          20             25             30
Gly Pro Glu Gly Val Gly Arg Arg Thr Val Ala Arg Trp Tyr Ala Trp
      35             40             45
Gly Leu Asn Arg Gly Phe Pro Pro Ser Leu Gly Glu His Pro Asp
      50             55             60
Val Leu Glu Val Gly Pro Lys Ala Arg Asp Leu Arg Gly Arg Ala Glu
      65             70             75             80
Val Arg Leu Glu Glu Val Ala Pro Leu Leu Glu Trp Cys Ser Ser His
          85             90             95
Pro Arg Glu Arg Val Lys Val Ala Ile Leu Asp Ser Ala His Leu Leu
      100             105             110
Thr Glu Ala Ala Ala Asn Ala Leu Leu Lys Leu Leu Glu Glu Pro Pro
      115             120             125
Ser Tyr Ala Arg Ile Val Leu Ile Ala Pro Ser Arg Ala Thr Leu Leu
      130             135             140
Pro Thr Leu Ala Ser Arg Ala Thr Glu Val Ala Phe Ala Pro Val Pro
      145             150             155             160
Glu Glu Ala Leu Arg Ala Leu Thr Gln Asp Pro Glu Leu Leu Arg Tyr
      165             170             175

```

Sequence_Listing_R10901_Corrected.txt

Ala Ala Gly Ala Pro Gly Arg Leu Leu Arg Ala Leu Gln Asp Pro Glu
180 185 190

Gly Tyr Arg Ala Arg Met Ala Arg Ala Gln Arg Val Leu Lys Ala Pro
195 200 205

Pro Leu Glu Arg Leu Ala Leu Leu Arg Glu Leu Leu Ala Glu Glu Glu
210 215 220

Gly Val His Ala Leu His Ala Val Leu Lys Arg Pro Glu His Leu Leu
225 230 235 240

Ala Leu Glu Arg Ala Arg Glu Ala Leu Glu Gly Tyr Val Ser Pro Glu
245 250 255

Leu Val Leu Ala Arg Leu Ala Leu Asp Leu Glu Thr
260 265

<210> 157
<211> 729
<212> DNA
<213> Thermus thermophilus

<400> 157
atgctggacc tggaggaggt gggggaggcg gagggaagc cctctaaagcc ccttttggaa 60
agcgtgcccg agggcgctcc cgtctctctc ctggacccta agccaagccc ctcccgggcg 120
gcctctacc ggaacccggg aaggcgggac ttcccccacc ccaaggggaa ggacctgggtg 180
cggcacctgg aaaacccggc caagcgcctg gggctcagcg tcccgggcgg ggtggcccg 240
tacctggcct cctctggagg ggacctcgag gcctggagc ggagctgga gaagcttgc 300
ctctctccc caccctcac cctggagaag gtggagaagg tggtgccct gaggccccc 360
ctcacgggct ttgacctggg cgcctcgtc ctggagaagg accccaagga gccctcctg 420
cgctaggcgc gcctcaagga ggagggggag gaggccctca ggtctctcg ggccctctc 480
tggcaggtcg cctctctcgc ccgggccttc ttctctctcc gggaaaaacc caggcccaag 540
gaggaggacc tcgcccgcct caggccccc cctacgcgc ccgcgcgcg cctggaggcg 600
gcgaagcgcc tcacggaaga ggcctcaag gaggccttg acgcccctat ggaggcgga 660
aagaggggca agggggggaa agaccgctg ctgcacctg agggcgcggt cctcgcctc 720
gccccgtga 729

<210> 158
<211> 292
<212> PRT
<213> Thermus thermophilus

<400> 158
Met Val Ile Ala Phe Thr Gly Asp Pro Phe Leu Ala Arg Glu Ala Leu
1 5 10 15

Leu Glu Glu Ala Arg Leu Arg Gly Leu Ser Arg Phe Thr Glu Pro Thr
20 25 30

Pro Glu Ala Leu Ala Gln Ala Leu Ala Pro Gly Leu Phe Gly Gly Gly
35 40 45

Gly Ala Met Leu Asp Leu Arg Glu Val Gly Glu Ala Glu Trp Lys Ala
50 55 60

Sequence_Listing_R10901_Corrected.txt

```

Leu Lys Pro Leu Leu Glu Ser Val Pro Glu Gly Val Pro Val Leu Leu
 65              70              75              80

Leu Asp Pro Lys Pro Ser Pro Ser Arg Ala Ala Phe Tyr Arg Asn Arg
              85              90              95

Glu Arg Arg Asp Phe Pro Thr Pro Lys Gly Lys Asp Leu Val Arg His
              100             105             110

Leu Glu Asn Arg Ala Lys Arg Leu Gly Leu Arg Leu Pro Gly Gly Val
 115              120              125

Ala Gln Tyr Leu Ala Ser Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg
 130              135              140

Glu Leu Glu Lys Leu Ala Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys
 145              150             155             160

Val Glu Lys Val Val Ala Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu
 165              170             175

Val Arg Ser Val Leu Glu Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu
 180              185             190

Gly Gly Leu Lys Glu Glu Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala
 195              200             205

Leu Ser Trp Gln Phe Ala Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg
 210              215             220

Glu Asn Pro Arg Pro Lys Glu Glu Asp Leu Ala Arg Leu Glu Ala His
 225              230             235             240

Pro Tyr Ala Ala Arg Arg Ala Leu Glu Ala Ala Lys Arg Leu Thr Glu
 245              250             255

Glu Ala Leu Lys Glu Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg
 260              265             270

Ala Lys Gly Gly Lys Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu
 275              280             285

Arg Leu Ala Arg
 290

```

<210> 159

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 159

gtgtgtcata tgagtaagga ttctgtccac cttcacc

37

<210> 160

Sequence_Listing_R10901_Corrected.txt

```

<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 160
gtgtgtggat cgggggacta ctgggaagta aggg              34

<210> 161
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 161
gtgtgtgcata tggaaaccac aatattccag ttccag            36

<210> 162
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 162
gtgtgtggat ccttatccac catgagaagt atttttcac          39

<210> 163
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 163
gtgtgtgcata tggaaaaagt ttttttggga aaaaactcca g      41

<210> 164
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 164
gtgtgtggat ccttaatcog cctgaaoggc taacg              35

```


Sequence_Listing_R10901_Corrected.txt

```

<210> 165
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 165
gtgtgtcata tgaactacgt tcccttcgcg agaaagtaca g          41

<210> 166
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 166
gtgtgtggat ccttaaaaca gcctcgcccc gctgga          36

<210> 167
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 167
gtgtgtcata tgcgcgttaa ggtggacagg gag          33

<210> 168
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 168
tgtgtctcga gtcattggcta caccctcacc ggcac          35

<210> 169
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 169
gtgtgtcata tgctcaataa ggtttttata ataggaaagac ttacggg          47

```

Sequence_Listing_R10901_Corrected.txt

<210> 170
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 170
gtgtggatcc ttaaaaaggt attcgctcct ctctcatcgg 39

<210> 171
<211> 807
<212> DNA
<213> *Thermus thermophilus*

<400> 171
atggctcag gcctgaacgg cgttttcctc atcggcgccc tcgccaccgg gccggacatg 60
cgctacaccc cggcgggggc cgcattttg gacctgaccc tcgccggtca ggacctgctt 120
ctttccgata acggggggga accggagggt tcctgggtacc accgggtgag gctcttaggc 180
cgccaggcgg agatgtgggg cgaacctctt gaccaagggc agctcgtctt cgtggagggc 240
cgccctggagt acgcgccagt ggaaggagg ggggagaagc ggagcgagct ccagatccgg 300
gcccgaactcc ggacccccct gacgaccggg ggaagaagcg ggccggaggac agccggggggc 360
agcccaagct ccgcgcggcc ctgaaccagg tcttctctat gggcaacctg acccgggacc 420
cggaactccg ctacaccccc cagggcaccc cgggtggccc gctgggacct gccgtgaacg 480
agcgcgcgcca gggggcgagg gaggcgcacc acttcgtgga ggttcaggcc tggcgcgacc 540
tggcgagatg ggccggccgag ctgagggaagg gcgacggcct tttcgtgac ggccaggttg 600
tgaacgactc ctggaccagg tccagcgggc agcggcgctt ccagacccgt gtggaggccc 660
tcaggctgga ggcgcgccacc cgtggacctg cccaggcctg cccaggccgg cggaacaggt 720
ccgcggaagt ccagacgggt ggggtggaca ttgacgaagg cttggaagac tttccgccc 780
aggaggattt gcggttttga gcacgaa 807

<210> 172
<211> 266
<212> PRT
<213> *Thermus thermophilus*

<400> 172
Met Ala Arg Gly Leu Asn Arg Val Phe Leu Ile Gly Ala Leu Ala Thr
1 5 10 15
Arg Pro Asp Met Arg Tyr Thr Pro Ala Gly Leu Ala Ile Leu Asp Leu
20 25 30
Thr Leu Ala Gly Gln Asp Leu Leu Leu Ser Asp Asn Gly Gly Glu Pro
35 40 45
Glu Val Ser Trp Tyr His Arg Val Arg Leu Leu Gly Arg Gln Ala Glu
50 55 60
Met Trp Gly Asp Leu Leu Asp Gln Gly Gln Leu Val Phe Val Glu Gly
65 70 75 80
Arg Leu Glu Tyr Arg Gln Trp Glu Arg Glu Gly Glu Lys Arg Ser Glu
85 90 95

Sequence Listing_R10901_Corrected.txt

Leu Gln Ile Arg Ala Asp Phe Leu Asp Pro Leu Asp Asp Arg Gly Lys
 100 105 110
 Lys Arg Ala Glu Asp Ser Arg Gly Gln Pro Arg Leu Arg Ala Ala Leu
 115 120 125
 Asn Gln Val Phe Leu Met Gly Asn Leu Thr Arg Asp Pro Glu Leu Arg
 130 135 140
 Tyr Thr Pro Gln Gly Thr Ala Val Ala Arg Leu Gly Leu Ala Val Asn
 145 150 155 160
 Glu Arg Arg Gln Gly Ala Glu Glu Arg Thr His Phe Val Glu Val Gln
 165 170 175
 Ala Trp Arg Asp Leu Ala Glu Trp Ala Ala Glu Leu Arg Lys Gly Asp
 180 185 190
 Gly Leu Phe Val Ile Gly Arg Leu Val Asn Asp Ser Trp Thr Ser Ser
 195 200 205
 Ser Gly Glu Arg Arg Phe Gln Thr Arg Val Glu Ala Leu Arg Leu Glu
 210 215 220
 Arg Pro Thr Arg Gly Pro Ala Gln Ala Cys Pro Gly Arg Arg Asn Arg
 225 230 235 240
 Ser Arg Gln Val Gln Thr Gly Gly Val Asp Ile Asp Glu Gly Leu Glu
 245 250 255
 Asp Phe Pro Pro Glu Glu Asp Leu Pro Phe
 260 265

<210> 173

<211> 992

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 173

aattccgaca ttccaattga atcgtttatt ccgcttgaaa aagaaggcaa gttgctcggt 60
 gatgtgaaaa gaccggggag catcgtaactg caggcgcgct ttttctctga aatcgtagaa 120
 aaactgccgc aacaaacggt ggaaatcgaa acggaagaca actttttgac gatcatccgc 180
 tcggggcact cagaattccg cctcaatggg ctaaaacgccg acgaatatcc gcgctcgccg 240
 caaatgtgaag aagaaaaacgt gtttcaaatc ccggctgatt tattgaaaac cgtgattcgg 300
 caaacgggtgt tcgccggtttc tacatcggaac acgcgcccaa tcttgacagg tgtcaactgg 360
 aaagttagaac atggcgagct tgtctgcaca gcgacgcaca gtcactcgctt agccatcgcc 420
 aaagttagaaa ttgagtcgga aaatgaagta tcatacaacg tgcctcatcc tcgaaaaagt 480
 cctaattgagc tcagcaaaat tttagatgac ggcaaccacc cggtagacat cgtcatgaca 540
 gccaatcaag tgcattttaa gccgagcac ctctcttct tttccgggt gcttgacggc 600
 aactatccgg agacggcccg cttagttcca acagaaaagca aaacgacct gatcgtcaat 660
 gcaaaagagt ttctcgagcg aatcgaccca gcgtctctgc ttgctcgaga aggaaggaaac 720
 aacgttgtga aactgacgac gcttctctga ggaatgctcg aaatttctc gatttctccg 780
 agatcgggaa agtgacggag cagctgcaaa cggagtctct tgaaggggaa gagttgaaca 840
 ttctgttcag cgcgaaatat atgatggacg cgttgccggc gcttgatgga acagacattt 900
 caaatcagct tcactggggc catcgccggc ttcctgttgc gcccgcttca accgattcga 960
 tgcttcagct cattttgcg gtgagaacat at 992

Sequence_Listing_R10901_Corrected.txt

<210> 174

<211> 334

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 174

```

Asn Ser Asp Ile Ser Ile Ile Glu Ser Phe Ile Pro Leu Glu Lys Glu
 1             5             10             15

Gly Lys Leu Leu Val Asp Val Lys Arg Pro Gly Ser Ile Val Leu Gln
      20             25             30

Ala Arg Phe Phe Ser Glu Ile Val Lys Lys Leu Pro Gln Gln Thr Val
      35             40             45

Glu Ile Glu Thr Glu Asp Asn Phe Leu Thr Ile Ile Arg Ser Gly His
      50             55             60

Ser Glu Phe Arg Leu Asn Gly Leu Asn Ala Asp Glu Tyr Pro Arg Leu
      65             70             75             80

Pro Gln Ile Glu Glu Glu Asn Val Phe Gln Ile Pro Ala Asp Leu Leu
      85             90             95

Lys Thr Val Ile Arg Gln Thr Val Phe Ala Val Ser Thr Ser Glu Thr
      100            105            110

Arg Pro Ile Leu Thr Gly Val Asn Trp Lys Val Glu His Gly Glu Leu
      115            120            125

Val Cys Thr Ala Thr Asp Ser His Arg Leu Ala Met Arg Lys Val Lys
      130            135            140

Ile Ile Glu Ser Glu Asn Glu Val Ser Tyr Asn Val Val Ile Pro Gly
      145            150            155            160

Lys Ser Leu Asn Glu Leu Ser Lys Ile Ile Leu Asp Asp Gly Asn His
      165            170            175

Pro Val Asp Ile Val Met Thr Ala Asn Gln Val Leu Phe Lys Ala Glu
      180            185            190

His Leu Leu Phe Phe Ser Arg Leu Leu Asp Gly Asn Tyr Pro Glu Thr
      195            200            205

Ala Arg Leu Ile Pro Thr Glu Ser Lys Thr Thr Met Ile Val Asn Ala
      210            215            220

Lys Glu Phe Leu Gln Ala Ile Asp Arg Ala Ser Leu Leu Ala Arg Glu
      225            230            235            240

Gly Arg Asn Asn Val Val Lys Leu Thr Thr Leu Pro Gly Gly Met Leu
      245            250            255

Glu Ile Ser Ser Ile Ser Pro Glu Ile Gly Lys Val Thr Glu Gln Leu
      260            265            270

Gln Thr Glu Ser Leu Glu Gly Glu Glu Leu Asn Ile Ser Phe Ser Ala
      275            280            285

```

Sequence_Listing_R10901_Corrected.txt

Lys Tyr Met Met Asp Ala Leu Arg Ala Leu Asp Gly Thr Asp Ile Gln
290 295 300

Ile Ser Phe Thr Gly Ala Met Arg Pro Phe Leu Leu Arg Pro Leu His
305 310 315 320

Thr Asp Ser Met Leu Gln Leu Ile Leu Pro Val Arg Thr Tyr
325 330

<210> 175

<211> 492

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 175

atgattaacc gcgtcatttt ggtcggcagg ttaacgagag atccggagtt gcgttacact 60
ccaagcggag tggctgttgc cagctttacg ctgcgggtca accgtccgtt tacaaatcag 120
cagggcggag gggaacggga tttattcaa tgtgtcgttt ggccggccca ggccgaaaac 180
gtcgccaact tttgaaaaa ggggagcttg gctggtgtcg atggccgact gcaaacccgc 240
agctatgaaa atcaagaagg tcggcgtgtg tacgtgacgg aagtgggtggc tgatagcgtc 300
caatttcttg agccgaaagg aacgagcgag cagcgagggg cgacagcagg cggctactat 360
ggggatccat tccattcgg gcaagatcag aaccaccaat atccgaacga aaaaggggtt 420
ggccgcacag atgacgatcc ttccgccaat gacggccagc cgatcgatat ttctgatgat 480
gatttgcggt tt 492

<210> 176

<211> 164

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 176

Met Ile Asn Arg Val Ile Leu Val Gly Arg Leu Thr Arg Asp Pro Glu
1 5 10 15

Leu Arg Tyr Thr Pro Ser Gly Val Ala Val Ala Thr Phe Thr Leu Ala
20 25 30

Val Asn Arg Pro Phe Thr Asn Gln Ser Tyr Glu Asn Gln Glu Gly Arg
35 40 45

Arg Val Tyr Val Thr Glu Val Val Ala Asp Ser Val Gln Phe Leu Glu
50 55 60

Pro Lys Gly Thr Ser Glu Gln Arg Gly Ala Thr Ala Gly Gly Tyr Tyr
65 70 75 80

Gln Gly Glu Arg Glu Thr Asp Phe Ile Gln Cys Val Val Trp Arg Arg
85 90 95

Gln Ala Glu Asn Val Ala Asn Phe Leu Lys Lys Gly Ser Leu Ala Gly
100 105 110

Val Asp Gly Arg Leu Gln Thr Arg Gly Asp Pro Phe Pro Phe Gly Gln
115 120 125

Asp Gln Asn His Gln Tyr Pro Asn Glu Lys Gly Phe Gly Arg Ile Asp

130

135

140

Asp Asp Pro Phe Ala Asn Asp Gly Gln Pro Ile Asp Ile Ser Asp Asp
 145 150 155 160

Asp Leu Pro Phe

<210> 177

<211> 1044

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 177

```

atgctggaac gcgtatgggg aaacattgaa aaacggcggt tttctccct ttatttatta 60
tacggcaatg agccgttttt attaacggaa acgtatgagc gatttggtgaa cgcagcgctt 120
ggccccgagg agcgggagtg gaacttgggt gtgtacgact gcgaggaaac gccgatcgag 180
gcggcgcttg aggaggccga gacggtgccg ttttccggcg agcggcggtgt catctccatc 240
aagcatccat atttttttac gtctgaaaaa gagaaggaga tcgaacatga tttggcggaag 300
ctggaggcgt aottgaaggg gccgtgcgag ttttcgatcg tctctctttt cgcgccgtac 360
gagaagcttg atgagcgaaa aaaaattacg aagctcgcca aagagcaaa cgaagtcgtc 420
atcgccgccc cgctcgccga agcggagctg cgtgcctggg tgcggcgccg catcgagagc 480
caagggggcg aagcaagcga cgaggcgatt gatgtcctgt tgcggcgggc cgggacgcag 540
ctttccgctt tggcgaatga aatcgataaa ttggccctgt ttgccggatc gggcggaacc 600
atcgaggcgg cggcggttga gcggtctgtc gcccgcaocg cggaagaaaa cgtatttgtg 660
cttgcgagc aagtggcgaa gcgcgacatt ccagcagcgt tgcagacgtt ttatgatctg 720
cttgaataca atgaagagcc gatcaaaatt ttggcgttgc tcgccgccca tttccgcttg 780
ctttcgcaag tgaatagggt tgcctcctta ggctacggac aggcgcaaat tgctgcggcg 840
ctcaagggtg acccggtccg cgtcaagctc gctcttgctc aagcgcccg cttcgctgac 900
ggagagcttg ctgagggcat caacgagctc gctgacggcg attacgaagt gaaaagcggg 960
gcggtcgatc gccggttgcc cgttgagctg cttctgatgc gctggggcgc cgcgccggcg 1020
caagcggggc gccacggccc gcgg

```

<210> 178

<211> 348

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 178

```

Met Leu Glu Arg Val Trp Gly Asn Ile Glu Lys Arg Arg Phe Ser Pro
  1 5 10 15
Leu Tyr Leu Leu Tyr Gly Asn Glu Pro Phe Leu Leu Thr Glu Thr Tyr
  20 25 30
Glu Arg Leu Val Asn Ala Ala Leu Gly Pro Glu Glu Arg Glu Trp Asn
  35 40 45
Leu Ala Val Tyr Asp Cys Glu Glu Thr Pro Ile Glu Ala Ala Leu Glu
  50 55 60
Glu Ala Glu Thr Val Pro Phe Phe Gly Glu Arg Arg Val Ile Leu Ile
  65 70 75 80
Lys His Pro Tyr Phe Phe Thr Ser Glu Lys Glu Lys Glu Ile Glu His
  85 90 95

```

Sequence_Listing_R10901_Corrected.txt

Asp Leu Ala Lys Leu Glu Ala Tyr Leu Lys Ala Pro Ser Pro Phe Ser
 100 105 110

Ile Val Val Phe Phe Ala Pro Tyr Glu Lys Leu Asp Glu Arg Lys Lys
 115 120 125

Ile Thr Lys Leu Ala Lys Glu Gln Ser Glu Val Val Ile Ala Ala Pro
 130 135 140

Leu Ala Glu Ala Glu Leu Arg Ala Trp Val Arg Arg Ile Glu Ser
 145 150 155 160

Gln Gly Ala Gln Ala Ser Asp Glu Ala Ile Asp Val Leu Leu Arg Arg
 165 170 175

Ala Gly Thr Gln Leu Ser Ala Leu Ala Asn Glu Ile Asp Lys Leu Ala
 180 185 190

Leu Phe Ala Gly Ser Gly Gly Thr Ile Glu Ala Ala Ala Val Glu Arg
 195 200 205

Leu Val Ala Arg Thr Pro Glu Glu Asn Val Phe Val Leu Val Glu Gln
 210 215 220

Val Ala Lys Arg Asp Ile Pro Ala Ala Leu Gln Thr Phe Tyr Asp Leu
 225 230 235 240

Leu Glu Asn Asn Glu Glu Pro Ile Lys Ile Leu Ala Leu Leu Ala
 245 250 255

His Phe Arg Leu Leu Ser Gln Val Lys Trp Leu Ala Ser Leu Gly Tyr
 260 265 270

Gly Gln Ala Gln Ile Ala Ala Ala Leu Lys Val His Pro Phe Arg Val
 275 280 285

Lys Leu Ala Leu Ala Gln Ala Ala Arg Phe Ala Asp Gly Glu Leu Ala
 290 295 300

Glu Ala Ile Asn Glu Leu Ala Asp Ala Asp Tyr Glu Val Lys Ser Gly
 305 310 315 320

Ala Val Asp Arg Arg Leu Ala Val Glu Leu Leu Met Arg Trp Gly
 325 330 335

Ala Arg Pro Ala Gln Ala Gly Arg His Gly Arg Arg
 340 345

<210> 179

<211> 757

<212> DNA

<213> Bacillus stearothermophilus

<400> 179

atgcgatggg aacagctagc gaaacgccag ccggtggtgg cgaaaatgct gcaaagcggc 60
 ttggaaaaag gccgatttc tcatgcgtac ttgtttgagg ggcagcgggg gacgggcaaa 120
 aaagcggcca gtttgtgtt gccgaaacgt ttgtttgtc tgcaccaat cggagtttc 180
 ccgtgtctag agtcgccgaa ctgccggcgc atcgactccg gcaaacccc tgacgtccgg 240

Sequence_Listing_R10901_Corrected.txt

```

gtgatcgccgagatggaggatcaatcaaaaaggaaacaaatcgatggctgcagcaagag300
ttctcgaaaaaacgcggtcgagtcgggataaaa aaatgtacatcggttgacacgccgatcaa360
atgacgacaaa gcgctgcgaacagccttctgaaatttttggaaagagccgcatccggggagc420
gtggcggttat tgcgtgactga gcaataccacgcctgctagggacgatcgttcccgctgt480
caagtgcctttcgttccggccgttgccgcgcgcgagagctcgcccagggacttgtcgaggag540
cacgtgcctgtgcctgtggcgtgtgttggtgccgccatttgaacaaacagcttcgagggaagca600
ctggcgcttgccaaagatagttggtttggcaggcgcgaaattagtgctacaatgggtat660
gagatgctgggcaagccggagctgcagctttgttttttcatcacgaccgcttgtttccg720
catttttttgaaagccatcagcttgaccttggacttg757

```

<210> 180

<211> 252

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 180

```

Met Arg Trp Glu Gln Leu Ala Lys Arg Gln Pro Val Val Ala Lys Met
 1          5          10         15

Leu Gln Ser Gly Leu Glu Lys Gly Arg Ile Ser His Ala Tyr Leu Phe
 20         25         30

Glu Gly Gln Arg Gly Thr Gly Lys Lys Ala Ala Ser Leu Leu Leu Ala
 35         40         45

Lys Arg Leu Phe Cys Leu Ser Pro Ile Gly Val Ser Pro Cys Leu Glu
 50         55         60

Cys Arg Asn Cys Arg Arg Ile Asp Ser Gly Asn His Pro Asp Val Arg
 65         70         75         80

Val Ile Gly Pro Asp Gly Gly Ser Ile Lys Lys Glu Gln Ile Glu Trp
 85         90         95

Leu Gln Gln Glu Phe Ser Lys Thr Ala Val Glu Ser Asp Lys Lys Met
100        105        110

Tyr Ile Val Glu His Ala Asp Gln Met Thr Thr Ser Ala Ala Asn Ser
115        120        125

Leu Leu Lys Phe Leu Glu Glu Pro His Pro Gly Thr Val Ala Val Leu
130        135        140

Leu Thr Glu Gln Tyr His Arg Leu Leu Gly Thr Ile Val Ser Arg Cys
145        150        155        160

Gln Val Leu Ser Phe Arg Pro Leu Pro Pro Ala Glu Leu Ala Gln Gly
165        170        175

Leu Val Glu Glu His Val Pro Leu Pro Leu Ala Leu Leu Ala Ala His
180        185        190

Leu Thr Asn Ser Phe Glu Glu Ala Leu Ala Leu Ala Lys Asp Ser Trp
195        200        205

Phe Ala Glu Ala Arg Thr Leu Val Leu Gln Trp Tyr Glu Met Leu Gly
210        215        220

```


Sequence Listing_R10901_Corrected.txt

Lys Pro Glu Leu Gln Leu Leu Phe Phe Ile His Asp Arg Leu Phe Pro
225 230 235 240

His Phe Leu Glu Ser His Gln Leu Asp Leu Gly Leu
245 250

<210> 181

<211> 1677

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 181

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tacttatttt cgggcccgcg cggtagacga aaaacgagcg cagcgaaaaat tttcgccaag 180
cgcggtcaact gtgaacacggc gccagcgggcg gagccatgca atgagtgctc agcttgccctc 240
ggcattacga atggaacggg tcccgatgtg ctggaaaattg acgctgcttc caacaaacggc 300
tcgatgaaaa ttctgtgatc cgtgagaaag gtgaaatttg cgcgcaacgtc ggcccgctcac 360
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aaaaacgttgg aggaacggcgc gaaacacgtc attttcattt tggccacgac cgagccgcac 480
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caggcgatcg ttccacggct aaagtacgtc gcaacgcccc aagggtgtcg ggcgtcagat 600
gaggcattgt ccgcacatgc ccgtgctgca gacgggggga tgcgcgatgc gtcagcttg 660
cttgatcaag ccatttcgtt cagcgacggg aaacttcggc tcgacgacgt gctggcgatg 720
accggggctg calcattlge cccttattcg agcttcacgc aagccatcca ccgcaaaagt 780
acagcggcggg ttcttcacga cttggaacag atgatggcgc aagggaagaag atcgcatcgt 840
ttggttgaa acctgatttt gtactatgc gatttattgc tgtacaaaac cgcctccat 900
tgaggaggcg cgattcaaat tgctgtcgtt gacgaagcgt tcacttcaat gtcggaaagt 960
attcgggttt ccaatttata cgaggccatc gacttgctga acaaaagcca gcaagagagt 1020
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tcagccgcgc ccccgctgct gtgcgcttcc gaattggaac cgttgataaa cgggattgaa 1140
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gcgcgcgtga aaaaactgtc caaacccgat aaaaacgggg gatataaagc cccggttggc 1260
cgcatttacg agctgttgaa acagcgcaag catgaagatt tagcttttgt gaaaggtatg 1320
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ttgtttgagc tgacaaaccc ccgctttgaa atggttagcca ttccggaggg aqaatgggga 1560
aaaaaagag aagagttcat ccgcaataag gacgcatagg tggaaaaaag cgaagaagat 1620
ccgttaatcg ccgaagcgaa gcggtgtgtt ggcgaagagc tgatcgaaat taaagaa 1677
```

<210> 182

<211> 559

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 182

Val Ala Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Ala
1 5 10 15

Asp Met Val Gly Gln Glu His Val Thr Lys Thr Leu Gln Ser Ala Leu
20 25 30

Leu Gln His Lys Ile Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys

Sequence_Listing_R10901_Corrected.txt

```

50                               55                               60
Glu Gln Ala Pro Ala Ala Glu Pro Cys Asn Glu Cys Pro Ala Cys Leu
65                               70                               75                               80
Gly Ile Thr Asn Gly Thr Val Pro Asp Val Leu Glu Ile Asp Ala Ala
85                               90                               95
Ser Asn Asn Arg Val Asp Glu Ile Arg Asp Ile Arg Glu Lys Val Lys
100                               105                               110
Phe Ala Pro Thr Ser Ala Arg Tyr Lys Val Tyr Ile Ile Asp Glu Val
115                               120                               125
His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130                               135                               140
Glu Pro Pro Lys His Val Ile Phe Ile Leu Ala Thr Thr Glu Pro His
145                               150                               155                               160
Lys Ile Pro Ala Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Arg
165                               170                               175
Arg Ile Pro Leu Gln Ala Ile Val Ser Arg Leu Lys Tyr Val Ala Ser
180                               185                               190
Ala Gln Gly Val Glu Ala Ser Asp Glu Ala Leu Ser Ala Ile Ala Arg
195                               200                               205
Ala Ala Asp Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala
210                               215                               220
Ile Ser Phe Ser Asp Gly Lys Leu Arg Leu Asp Asp Val Leu Ala Met
225                               230                               235                               240
Thr Gly Ala Ala Ser Phe Ala Ala Leu Ser Ser Phe Ile Glu Ala Ile
245                               250                               255
His Arg Lys Asp Thr Ala Ala Val Leu Gln His Leu Glu Thr Met Met
260                               265                               270
Ala Gln Gly Lys Asp Pro His Arg Leu Val Glu Asp Leu Ile Leu Tyr
275                               280                               285
Tyr Arg Asp Leu Leu Leu Tyr Lys Thr Ala Pro Tyr Val Glu Gly Ala
290                               295                               300
Ile Gln Ile Ala Val Val Asp Glu Ala Phe Thr Ser Leu Ser Glu Met
305                               310                               315                               320
Ile Pro Val Ser Asn Leu Tyr Glu Ala Ile Glu Leu Leu Asn Lys Ser
325                               330                               335
Gln Gln Glu Met Lys Trp Thr Asn His Pro Arg Leu Leu Glu Val
340                               345                               350
Ala Leu Val Lys Leu Cys His Pro Ser Ala Ala Ala Pro Ser Leu Ser
355                               360                               365

```

Sequence Listing_R10901_Corrected.txt

Ala Ser Glu Leu Glu Pro Leu Ile Lys Arg Ile Glu Thr Leu Glu Ala
 370 375 380

Glu Leu Arg Arg Leu Lys Glu Gln Pro Pro Ala Pro Pro Ser Thr Ala
 385 390 395 400

Ala Pro Val Lys Lys Leu Ser Lys Pro Met Lys Thr Gly Gly Tyr Lys
 405 410 415

Ala Pro Val Gly Arg Ile Tyr Glu Leu Lys Gln Ala Thr His Glu
 420 425 430

Asp Leu Ala Leu Val Lys Gly Cys Trp Ala Asp Val Leu Asp Thr Leu
 435 440 445

Lys Arg Gln His Lys Val Ser His Ala Ala Leu Leu Gln Glu Ser Glu
 450 455 460

Pro Val Ala Ala Ser Ala Ser Ala Phe Val Leu Lys Phe Lys Tyr Glu
 465 470 475 480

Ile His Cys Lys Met Ala Thr Asp Pro Thr Ser Ser Val Lys Glu Asn
 485 490 495

Val Glu Ala Ile Leu Phe Glu Leu Thr Asn Arg Arg Phe Glu Met Val
 500 505 510

Ala Ile Pro Glu Gly Glu Trp Gly Lys Ile Arg Glu Glu Phe Ile Arg
 515 520 525

Asn Lys Asp Ala Met Val Glu Lys Ser Glu Glu Asp Pro Leu Ile Ala
 530 535 540

Glu Ala Lys Arg Leu Phe Gly Glu Glu Leu Ile Glu Ile Lys Glu
 545 550 555

<210> 183

<211> 4301

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 183

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 gaggagcaaaa gctggcattt ttattttcag ttcgacaacg tgcctgccgt tcatgtatac 180
 aaaaactttg ccgatcggtc gcagacggcg ttccgccata tcgcccgcgt ccgccatacg 240
 atgagcgtgc aagcgcgcgc cgttaactgag gcgagatgtc aggcgtattg ccgcgtttgc 300
 ctgcccagag tgcaagaagg catgtccgcg ctgtgcgatt ggcctcagcg gcagagccct 360
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 aaacggcggg tcgccaaaaa aatcgctgat gtgtacgctt cgtttgggtt tccccccctt 480
 cagcttgacg tcagcgtcga gccgtccaag caagaaatgg aacagttttt ggccgcaaaaa 540
 cagcaagagg acgaagagcg agcgcgttgc gtactgacgc atttagcgag ggaagaagaa 600
 aagcgcgcgt ctgcgcgcgc gtcgggtccg ctgtcatcag gctatccgat ccgcagcag 660
 gagccggctg gccgcgcttg aacgatcgtc gaagaagagc gccgcgtcgt tgtgcaaggc 720
 tatgtatttg acgcgaagt gagcgaatta aaaaagcgcc gcaagcgtgt gaccatgaaa 780
 atcacagatt acacgaactc gattttagtc aaaaatgtct ccgcgcgaca agaggacgcc 840
 gagcttatga gccgcgtcaa aaaaggcatg tgggtgaaa tgccgcgcag cgtgcacaa 900
 gatacgttcg tccgtgattt ggtcatcatc gccaacgatt tgaacgaat ccgcgcaaac 960

Sequence Listing_R10901_Corrected.txt

```

gaacggcgaag atacggcgccg ggaaggggaa aagagggtcg agctccattt gcatacccc 1020
atgagccaaa tggacgcgggt cactccggtg acaaaactca ttgagcaagc gaaaaaatgt 1080
gggcatccgg cgatcccggt caccgacacc catcgaggtc agtcgtttcc ggagggcctac 1140
agcgccggcga aaaaacacgg catgaaagtc atttacggcc ttgaggcgaa catcgctcgac 1200
gatggcgctg cgatcgccca caatgagacg caccgcccgc ttccggagga aacgtgactgc 1260
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gatttgaaaa accatcggtt caatacattg tgcaaaaaat ttgacattga attgacgcag 1680
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gccttgactc gcttcagac cataaccagc tgcgtcgtt t 4301

```

Sequence_Listing_R10901_Corrected.txt

<211> 1433

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 184

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Met Val Thr Lys Glu Gln Lys Glu Arg Phe Leu Ile Leu Leu Glu Gln
 1          5          10          15

Leu Lys Met Thr Ser Asp Glu Trp Met Pro His Phe Arg Glu Ala Ala
 20          25          30

Ile Arg Lys Val Val Ile Asp Lys Glu Glu Lys Ser Trp His Phe Tyr
 35          40          45

Phe Gln Phe Asp Asn Val Leu Pro Val His Val Tyr Lys Thr Phe Ala
 50          55          60

Asp Arg Leu Gln Thr Ala Phe Arg His Ile Ala Ala Val Arg His Thr
 65          70          75          80

Met Glu Val Glu Ala Pro Arg Val Thr Glu Ala Asp Val Gln Ala Tyr
 85          90          95

Trp Pro Leu Cys Leu Ala Glu Leu Gln Glu Gly Met Ser Pro Leu Val
100          105          110

Asp Trp Leu Ser Arg Gln Thr Pro Glu Leu Lys Gly Asn Lys Leu Leu
115          120          125

Val Val Ala Arg His Glu Ala Glu Ala Leu Ala Ile Lys Arg Arg Phe
130          135          140

Ala Lys Lys Ile Ala Asp Val Tyr Ala Ser Phe Gly Phe Pro Pro Leu
145          150          155          160

Gln Leu Asp Val Ser Val Glu Pro Ser Lys Gln Glu Met Glu Gln Phe
165          170          175

Leu Ala Gln Lys Gln Gln Glu Asp Glu Glu Arg Ala Leu Ala Val Leu
180          185          190

Thr Asp Leu Ala Arg Glu Glu Glu Lys Ala Ala Ser Ala Pro Pro Ser
195          200          205

Gly Pro Leu Val Ile Gly Tyr Pro Ile Arg Asp Glu Glu Pro Val Arg
210          215          220

Arg Leu Glu Thr Ile Val Glu Glu Glu Arg Arg Val Val Val Gln Gly
225          230          235          240

Tyr Val Phe Asp Ala Glu Val Ser Glu Leu Lys Ser Gly Arg Thr Leu
245          250          255

Leu Thr Met Lys Lys Ile Thr Asp Tyr Thr Asn Ser Ile Leu Val Lys Met
260          265          270

Phe Ser Arg Asp Lys Glu Asp Ala Glu Leu Met Ser Gly Val Lys Lys
275          280          285

```

Sequence_Listing_R10901_Corrected.txt

Gly Met Trp Val Lys Val Arg Gly Ser Val Gln Asn Asp Thr Phe Val
 290 295 300

Arg Asp Leu Val Ile Ile Ala Asn Asp Leu Asn Glu Ile Ala Ala Asn
 305 310 315 320

Glu Arg Gln Asp Thr Ala Pro Glu Gly Glu Lys Arg Val Glu Leu His
 325 330 335

Leu His Thr Pro Met Ser Gln Met Asp Ala Val Thr Ser Val Thr Lys
 340 345 350

Leu Ile Glu Gln Ala Lys Lys Trp Gly His Pro Ala Ile Ala Val Thr
 355 360 365

Asp His Ala Val Val Gln Ser Phe Pro Glu Ala Tyr Ser Ala Ala Lys
 370 375 380

Lys His Gly Met Lys Val Ile Tyr Gly Leu Glu Ala Asn Ile Val Asp
 385 390 395 400

Asp Gly Val Pro Ile Ala Tyr Asn Glu Thr His Arg Arg Leu Ser Glu
 405 410 415

Glu Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val
 420 425 430

Tyr Asn Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Asp Gly Glu
 435 440 445

Ile Ile Asp Arg Phe Met Ser Phe Ala Asn Pro Gly His Pro Leu Ser
 450 455 460

Val Thr Thr Met Glu Leu Thr Gly Ile Thr Asp Glu Met Val Lys Asp
 465 470 475 480

Ala Pro Lys Pro Asp Glu Val Leu Ala Arg Phe Val Asp Trp Ala Gly
 485 490 495

Asp Ala Thr Leu Val Ala His Asn Ala Ser Phe Asp Ile Gly Phe Leu
 500 505 510

Asn Ala Gly Leu Ala Arg Met Gly Arg Gly Lys Ile Ala Asn Pro Val
 515 520 525

Ile Asp Thr Leu Glu Leu Ala Arg Phe Leu Tyr Pro Asp Leu Lys Asn
 530 535 540

His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
 545 550 555 560

His His Arg Ala Ile Tyr Asp Ala Glu Ala Thr Gly His Leu Leu Met
 565 570 575

Arg Leu Leu Lys Glu Ala Glu Glu Arg Gly Ile Leu Phe His Asp Glu
 580 585 590

Leu Asn Ser Arg Thr His Ser Glu Ala Ser Tyr Arg Leu Ala Arg Pro
 595 600 605

Sequence_Listing_R10901_Corrected.txt

```

Phe His Val Thr Leu Leu Ala Gln Asn Glu Thr Gly Leu Lys Asn Leu
610 615 620

Phe Lys Leu Val Ser Leu Ser His Ile Gln Tyr Phe His Arg Val Pro
625 630 635 640

Arg Ile Pro Arg Ser Val Leu Val Lys His Arg Asp Gly Leu Leu Val
645 650 655

Gly Ser Gly Cys Asp Lys Gly Glu Leu Phe Asp Asn Leu Ile Gln Lys
660 665 670

Ala Pro Glu Glu Val Glu Asp Ile Ala Arg Phe Tyr Asp Phe Leu Glu
675 680 685

Val His Pro Pro Asp Val Tyr Lys Pro Leu Ile Glu Met Asp Tyr Val
690 695 700

Lys Asp Glu Glu Met Ile Lys Asn Ile Ile Arg Ser Ile Val Ala Leu
705 710 715 720

Gly Glu Lys Leu Asp Ile Pro Val Val Ala Thr Gly Asn Val His Tyr
725 730 735

Leu Asn Pro Glu Asp Lys Ile Tyr Arg Lys Ile Leu Ile His Ser Gln
740 745 750

Gly Gly Ala Asn Pro Leu Asn Arg His Glu Leu Pro Asp Val Tyr Phe
755 760 765

Arg Thr Thr Asn Glu Met Leu Asp Cys Phe Ser Phe Leu Gly Pro Glu
770 775 780

Lys Ala Lys Glu Ile Val Val Asp Asn Thr Gln Lys Ile Ala Ser Leu
785 790 795 800

Ile Gly Asp Val Lys Pro Ile Lys Asp Glu Leu Tyr Thr Pro Arg Ile
805 810 815

Glu Gly Ala Asp Glu Glu Ile Arg Glu Met Ser Tyr Arg Arg Ala Lys
820 825 830

Glu Ile Tyr Gly Asp Pro Leu Pro Lys Leu Val Glu Glu Arg Leu Glu
835 840 845

Lys Glu Leu Lys Ser Ile Ile Gly His Gly Phe Ala Val Ile Tyr Leu
850 855 860

Ile Ser His Lys Leu Val Lys Lys Ser Leu Asp Asp Gly Tyr Leu Val
865 870 875 880

Gly Ser Arg Gly Ser Val Gly Ser Ser Phe Val Ala Thr Met Thr Glu
885 890 895

Ile Thr Glu Val Asn Pro Leu Pro Pro His Tyr Val Cys Pro Asn Cys
900 905 910

Lys His Ser Glu Phe Phe Asn Asp Gly Ser Val Gly Ser Gly Phe Asp

```

Sequence_Listing_R10901_Corrected.txt

```

915                               920                               925
Leu Pro Asp Lys Asn Cys Pro Arg Cys Gly Thr Lys Tyr Lys Lys Asp
930                               935                               940

Gly His Asp Ile Pro Phe Glu Thr Phe Leu Gly Phe Lys Gly Asp Lys
945                               950                               955                               960

Val Pro Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Pro Arg Ala
965                               970                               975

His Asn Tyr Thr Lys Val Leu Phe Gly Glu Asp Asn Val Tyr Arg Ala
980                               985                               990

Gly Thr Ile Gly Thr Val Ala Asp Lys Thr Ala Tyr Gly Phe Val Lys
995                               1000                               1005

Ala Tyr Ala Ser Asp His Asn Leu Glu Leu Arg Gly Ala Glu Ile Asp
1010                               1015                               1020

Leu Ala Ala Gly Cys Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro
1025                               1030                               1035                               1040

Gly Gly Ile Ile Val Val Pro Asp Tyr Met Glu Ile Tyr Asp Phe Thr
1045                               1050                               1055

Pro Ile Gln Tyr Pro Ala Asp Asp Thr Ser Ser Glu Trp Arg Thr Thr
1060                               1065                               1070

His Phe Asp Phe His Ser Ile His Asp Asn Leu Leu Lys Leu Asp Ile
1075                               1080                               1085

Leu Gly His Asp Asp Pro Thr Val Ile Arg Met Leu Gln Asp Leu Ser
1090                               1095                               1100

Gly Ile Asp Pro Lys Thr Ile Pro Thr Asp Asp Pro Asp Val Met Gly
1105                               1110                               1115                               1120

Ile Phe Ser Ser Thr Glu Pro Leu Gly Val Thr Pro Glu Gln Ile Met
1125                               1130                               1135

Cys Asn Val Gly Thr Ile Gly Ile Pro Glu Phe Gly Thr Arg Phe Val
1140                               1145                               1150

Arg Gln Met Leu Glu Glu Thr Arg Pro Lys Thr Phe Ser Glu Leu Val
1155                               1160                               1165

Gln Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Gly Asn Ala
1170                               1175                               1180

Gln Glu Leu Ile Gln Asn Gly Thr Cys Thr Leu Ser Glu Val Ile Gly
1185                               1190                               1195                               1200

Cys Arg Asp Asp Ile Met Val Tyr Leu Ile Tyr Arg Gly Leu Glu Pro
1205                               1210                               1215

Ser Leu Ala Phe Lys Ile Met Glu Ser Val Arg Lys Gly Lys Gly Leu
1220                               1225                               1230

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Sequence Listing_R10901_Corrected.txt

Thr Pro Glu Phe Glu Ala Glu Met Arg Lys His Asp Val Pro Glu Trp
1235 1240 1245

Tyr Ile Asp Ser Cys Lys Lys Ile Lys Tyr Met Phe Pro Lys Ala His
1250 1255 1260

Ala Ala Ala Tyr Val Leu Met Ala Val Arg Ile Ala Tyr Phe Lys Val
1265 1270 1275 1280

His His Pro Leu Leu Tyr Tyr Ala Ser Tyr Phe Thr Val Arg Ala Glu
1285 1290 1295

Asp Phe Asp Leu Asp Ala Met Ile Lys Gly Ser Pro Ala Ile Arg Lys
1300 1305 1310

Arg Ile Glu Glu Ile Asn Ala Lys Gly Ile Gln Ala Thr Ala Lys Glu
1315 1320 1325

Lys Ser Leu Leu Thr Val Leu Glu Val Ala Leu Glu Met Cys Glu Arg
1330 1335 1340

Gly Phe Ser Phe Lys Asn Ile Asp Leu Tyr Arg Ser Gln Ala Thr Glu
1345 1350 1355 1360

Phe Val Ile Asp Gly Asn Ser Leu Ile Pro Pro Phe Asn Ala Ile Pro
1365 1370 1375

Gly Leu Gly Thr Asn Val Ala Gln Ala Ile Val Arg Ala Arg Glu Glu
1380 1385 1390

Gly Glu Phe Leu Ser Lys Glu Asp Leu Gln Gln Arg Gly Lys Leu Ser
1395 1400 1405

Lys Thr Leu Leu Glu Tyr Leu Glu Ser Arg Gly Cys Leu Asp Ser Leu
1410 1415 1420

Pro Asp His Asn Gln Leu Ser Leu Phe
1425 1430

<210> 185

<211> 199

<212> PRT

<213> Thermus thermophilus

<400> 185

Thr Pro Lys Gly Lys Asp Leu Val Arg His Leu Glu Asn Arg Ala Lys
1 5 10 15

Arg Leu Gly Leu Arg Leu Pro Gly Gly Val Ala Gln Tyr Leu Ala Ser
20 25 30

Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala
35 40 45

Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala
50 55 60

Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu
Page 129

Sequence_Listing_R10901_Corrected.txt

```

65          70          75          80
Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu Gly Arg Leu Lys Glu Glu
      85          90          95
Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala
      100         105         110
Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg Glu Met Pro Arg Pro Lys
      115         120         125
Glu Glu Asp Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys
      130         135         140
Ala Leu Leu Glu Ala Ala Arg Arg Leu Thr Glu Glu Ala Leu Lys Glu
      145         150         155         160
Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg Ala Lys Gly Gly Lys
      165         170         175
Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu Arg Leu Ala Arg Pro
      180         185         190
Ala Gly Gln Pro Arg Val Asp
      195

```

<210> 186

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 186

gcccagtagc tcgctccct cgagggg

27

<210> 187

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 187

ggcccccttg gcctctcgg cctccat

27

<210> 188

<211> 331

<212> DNA

<213> Thermus thermophilus

<400> 188

agactcgagg cctcgagcg ggagctggag aagcttgccc tctctcccc accctcacc 60
ctggagaagg tggagaagg gtggccctg agggccccc tcacgggett tgacctggg 120

Sequence Listing_R10901_Corrected.txt

```
cgctccgtcc tggagaagga ccccaaggag gccctcctgc gccacaggcg cctcagggag 180
gagggggagg agccctccag gctcctcggg gccctctect gccagttcgc cctcctcgcc 240
cgggccttct tctcctccg ggaaccacc aggcccaagg agggaggacct cgcccgctc 300
gaggcccaac cctacgcgc caagaaggcc a 331
```

<210> 189
<211> 110
<212> PRT
<213> Thermus thermophilus

```
<400> 189
Arg Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala Leu Leu Ser
 1          5          10          15

Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala Leu Arg Pro
 20          25          30

Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu Lys Asp Pro
 35          40          45

Lys Glu Ala Leu Leu Arg Leu Arg Arg Leu Arg Glu Glu Gly Glu Glu
 50          55          60

Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala Leu Leu Ala
 65          70          75          80

Arg Ala Phe Phe Leu Leu Arg Glu Asn Pro Arg Pro Lys Glu Glu Asp
 85          90          95

Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys Ala
100          105          110
```

<210> 190
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

```
<400> 190
gtggtgtcta gacatcataa cgggtctggc a 31
```

<210> 191
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

```
<400> 191
gagggccacc acctctcca cctctc 27
```

<210> 192

Sequence_Listing_R10901_Corrected.txt

```

<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 192
ctccgtcctg gagaaggacc ccaag                25

<210> 193
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<221> primer_bind
<222> (15)
<223> S at position 15 can be either C or G

<220>
<221> primer_bind
<222> (27)
<223> S at position 27 can be either C or G

<400> 193
cgcgaaattca acgcctcctc caagacsct          29

<210> 194
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 194
gacacttaac atatggtcat cgcccttcacc g        31

<210> 195
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 195
gtgtgtgaat tcgggtcaac gggcgaggcg gaggaccg  38

<210> 196
<211> 10

```

Sequence_Listing_R10901_Corrected.txt

<212> PRT

<213> *Deinococcus radiodurans*

<400> 196

Val Ile Leu Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 197

<211> 10

<212> PRT

<213> *Methanococcus jannaschii*

<400> 197

Tyr Leu Ile Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 198

<211> 10

<212> PRT

<213> *Thermotoga maritima*

<400> 198

Leu Val Leu Asn Pro Gly Ser Ala Gly Arg
1 5 10

<210> 199

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 199

ctgggtgaacc cgggctccgt gggccagc

28

<210> 200

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 200

Leu Leu Val Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 201

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 201
ctcgaggagc ttgaggagg tggtggc

27

<210> 202
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 202
Ala Asn Thr Leu Leu Lys Leu Leu Glu
1 5

<210> 203
<211> 32
<212> PRT
<213> Deinococcus radiodurans

<400> 203
Gly Phe Gly Gly Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Leu Ser Pro Arg His Asn Val Arg Glu Asp Glu Tyr Gly Gly
20 25 30

<210> 204
<211> 32
<212> PRT
<213> Caenorhabditis elegans

<400> 204
Gly Phe Asp Gly Ile Gln Leu His Gly Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Thr Ser Pro Thr Thr Asn Lys Arg Val Asp Lys Tyr Gly Gly
20 25 30

<210> 205
<211> 32
<212> PRT
<213> Pseudomonas aeruginosa

<400> 205
Gly Phe Ser Gly Val Glu Ile His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Sequence_Listing_R10901_Corrected.txt

Gln Phe Leu Ser Pro Leu Ser Asn Arg Arg Ser Asp Ala Trp Gly Gly
20 25 30

<210> 206
<211> 32
<212> PRT
<213> Archaeoglobus fulgidus

<400> 206
Gly Phe Asp Ala Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Glu Phe Ile Ser Pro His Val Asn Arg Arg Lys Asp Glu Tyr Gly Gly
20 25 30

<210> 207
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 207
catcctggac tcggccacc tctcaccga 30

<210> 208
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 208
Ile Leu Asp Ser Ala His Leu Leu Thr
1 5

<210> 209
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 209
gaggaggtag ccgtgggccc cgtggagctc cac 33

Sequence_Listing_R10901_Corrected.txt

```

<210> 210
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 210
Val Glu Leu His Ala Ala His Gly Tyr Leu Leu
  1             5             10

<210> 211
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 211
ggctttccca tatggtctca caccggctc ac
                                         32

<210> 212
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 212
gcgtggatcc acggtcatgt ctctaagtc
                                         29

```